FIG. 1

ATGACGTCCACCTGCACCAACAGCACGCGCGAGAGTAACAGCAGCCACACGTGCATGCCC
CTCTCCAAAATGCCCATCAGCCTGGCCCACGGCATCATCCGCTCAACCGTGCTGGTTATC
TTCCTCGCCGCCTCTTTCGTCGGCAACATAGTGCTGGCGCTAGTGTTGCAGCGCAAGCCG
CAGCTGCTGCAGGTGACCAACCGTTTTATCTTTAACCTCCTCGTCACCGACCTGCTGCAG
ATTTCGCTCGTGGCCCCCTGGGTGGTGGCCACCTCTGTGCCTCTCTTCTGGCCCCTCAAC
AGCCACTTCTGCACGGCCCTGGTTAGCCTCACCCACCTGTTCGCCTTCGCCAGCGTCAAC
ACCATTGTCTTGGTGTCAGTGGATCGCTACTTGTCCATCATCCACCCTCTCTCCTACCCG
TCCAAGATGACCCAGCGCCGCGGTTACCTGCTCCTCTATGGCACCTGGATTGTGGCCATC
CTGCAGAGCACTCCTCCACTCTACGGCTGGGGCCAGGCTGCCTTTGATGAGCGCAATGCT
CTCTGCTCCATGATCTGGGGGGCCAGCCCCAGCTACACTATTCTCAGCGTGGTGTCCTTC
ATCGTCATTCCACTGATTGTCATGATTGCCTGCTACTCCGTGGTGTTCTGTGCAGCCCGG
AGGCAGCATGCTCTGCTGTACAATGTCAAGAGACACAGCTTGGAAGTGCGAGTCAAGGAC
TGTGTGGAGAATGAGGATGAAGAGGGAGCAGAGAAGAAGGAGGAGTTCCAGGATGAGAGT
GAGTTTCGCCGCCAGCATGAAGGTGAGGTCAAGGCCAAGGAGGGCAGAATGGAAGCCAAG
GACGGCAGCCTGAAGGCCAAGGAAGGAAGCACGGGGACCAGTGAGAGTAGTGTAGAGGCC
AGGGGCAGCGAGGAGGTCAGAGAGAGCAGCACGGTGGCCAGCGACGGCAGCATGGAGGGT
AAGGAAGGCAGCACCAAAGTTGAGGAGAACAGCATGAAGGCAGACAAGGGTCGCACAGAG
GTCAACCAGTGCAGCATTGACTTGGGTGAAGATGACATGGAGTTTGGTGAAGACGACATC
AATTTCAGTGAGGATGACGTCGAGGCAGTGAACATCCCGGAGAGCCTCCCACCCAGTCGT
CGTAACAGCAACAGCAACCCTCCTCTGCCCAGGTGCTACCAGTGCAAAGCTGCTAAAGTG
ATCTTCATCATCATTTTCTCCTATGTGCTATCCCTGGGGCCCTACTGCTTTTTAGCAGTC
CTGGCCGTGTGGGTGGATGTCGAAACCCAGGTACCCCAGTGGGTGATCACCATAATCATC
TGGCTTTTCTTCCTGCAGTGCTGCATCCACCCCTATGTCTATGGCTACATGCACAAGACC
ATTAAGAAGGAAATCCAGGACATGCTGAAGAAGTTCTTCTGCAAGGAAAAGCCCCCGAAA
GAAGATAGCCACCCAGACCTGCCCGGAACAGAGGGTGGGACTGAAGGCAAGATTGTCCCT
TCCTACGATTCTGCTACTTTTCCTTGA

FIG. 2

MTSTCTNSTRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKP
QLLQVTNRFIFNLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVN
TIVLVSVDRYLSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNA
LCSMIWGASPSYTILSVVSFIVIPLIVMIACYSVVFCAARRQHALLYNVKRHSLEVRVKD
CVENEDEEGAEKKEEFQDESEFRRQHEGEVKAKEGRMEAKDGSLKAKEGSTGTSESSVEA
RGSEEVRESSTVASDGSMEGKEGSTKVEENSMKADKGRTEVNQCSIDLGEDDMEFGEDDI
NFSEDDVEAVNIPESLPPSRRNSNSNPPLPRCYQCKAAKVIFIIIFSYVLSLGPYCFLAV
LAVWVDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQDMLKKFFCKEKPPK
EDSHPDLPGTEGGTEGKIVPSYDSATFP

FIG. 3

GCAACCTGTCTCACGCCCTCTGGCTGTTGCC

FIG. 4

AGTTAGTTCTAAGGCAAACCTT

FIG. 5

```
  1  MTSTCTNSTR ESNSSHTCMP LSKMPISLAH GIIRSTVLVI FLAASFVGNI
 51  VLALVLQRKP QLLQVTNRFI FNLLVTDLLQ ISLVAPWVVA TSVPLFWPLN
101  SHFCTALVSL THLFAFASVN TIVLVSVDRY LSIIHPLSYP SKMTQRRGYL
151  LLYGTWIVAI LQSTPPLYGW GQAAFDERNA LCSMIWGASP SYTILSVVSF
201  IVIPLIVMIA CYSVVFCAAR RQHALLYNVK RHSLEVRVKD CVENEDEEGA
251  EKKEEFQDES EFRRQHEGEV KAKEGRMEAK DGSLKAKEGS TGTSESSVEA
301  RGSEEVRESS TVASDGSMEG KEGSTKVEEN SMKADKGRTE VNQCSIDLGE
351  DDMEFGEDDI NFSEDDVEAV NIPESLPPSR RNSNSNPPLP RCYQCKAAKV
401  IFIIIFSYVL SLGPYCFLAV LAVWVDVETQ VPQWVITIII WLFFLQCCIH
451  PYVYGYMHKT IKKEIQDMLK KFFCKEKPPK EDSHPDLPGT EGGTEGKIVP
501  SYDSATFP
```

FIG. 6A


ACM4_CHICK
YDBM_CAEEL
5H1A_HUMAN
5H1A_MOUSE
5H1A_FUGRU
5HT_LYMST
A1AD_HUMAN
A1AD_MOUSE
Q13675
Q13729
O60451
A1AA_RAT
O54913
A1AA_BOVIN
A1AA_CANFA
A1AA_RABIT
A1AA_HUMAN
A1AA_ORYLA
O96716
O75963
HGPRBMY8

FIG. 6B

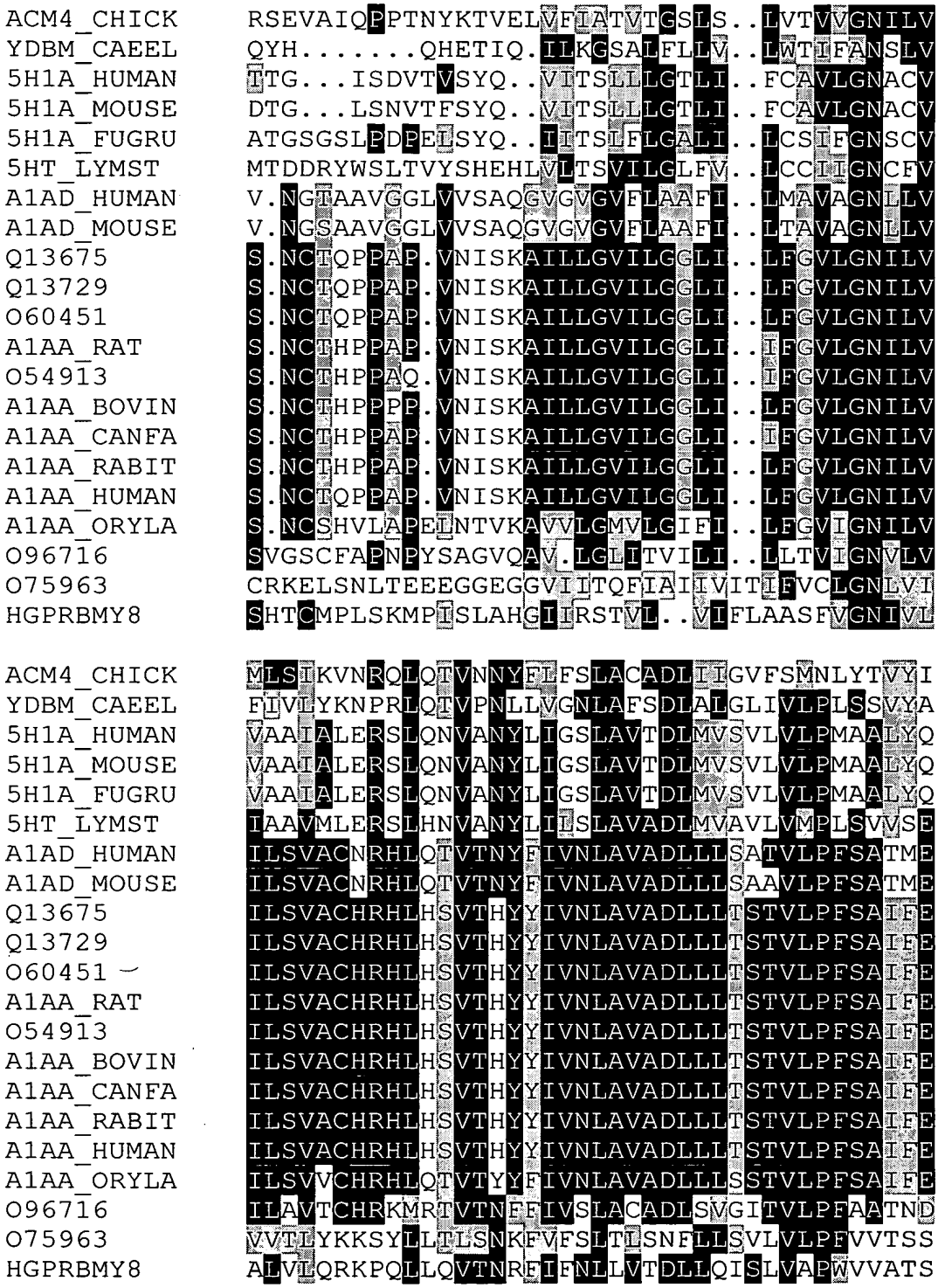
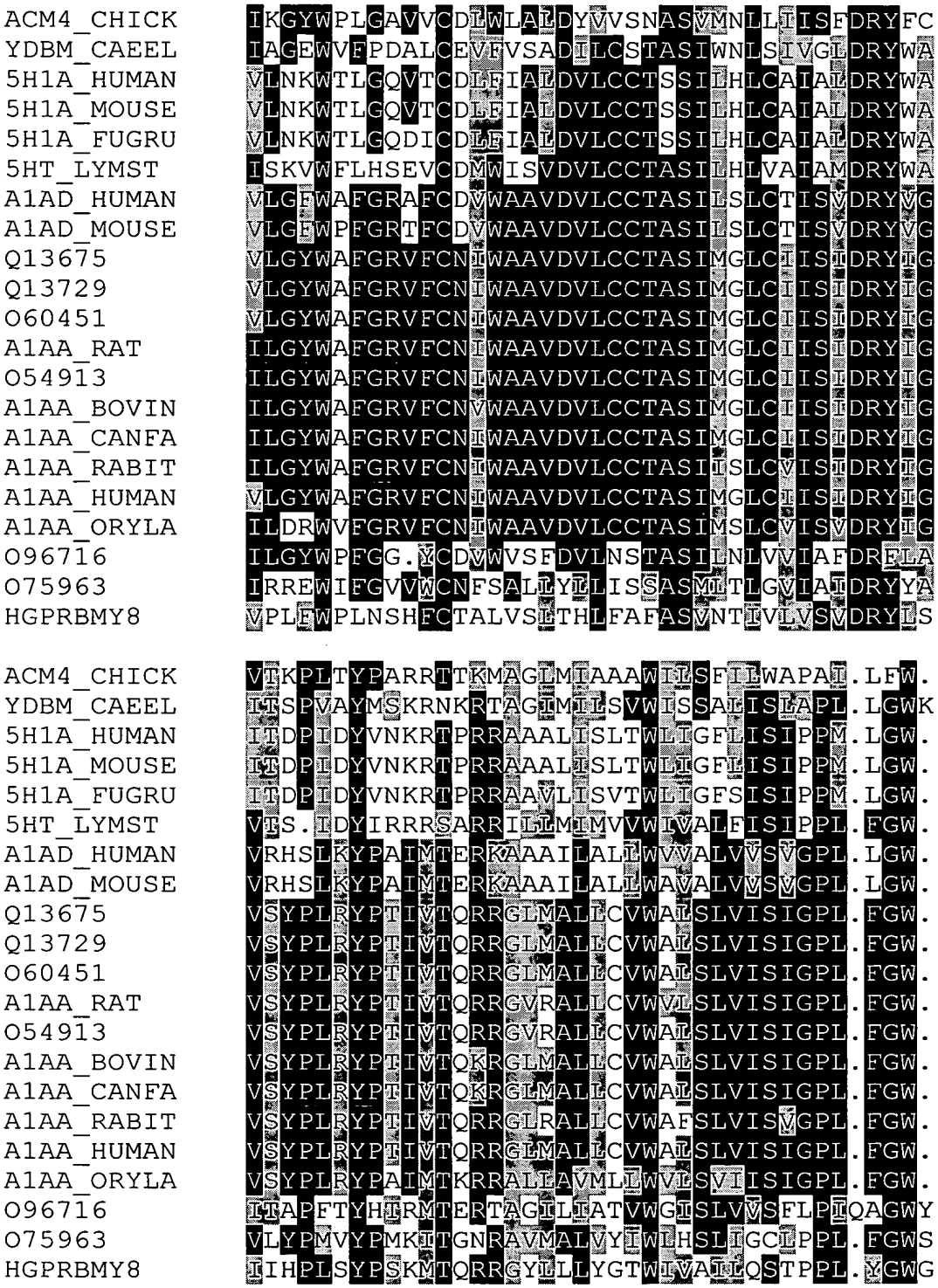

ACM4_CHICK
YDBM_CAEEL
5H1A_HUMAN
5H1A_MOUSE
5H1A_FUGRU
5HT_LYMST
A1AD_HUMAN
A1AD_MOUSE
Q13675
Q13729
O60451
A1AA_RAT
O54913
A1AA_BOVIN
A1AA_CANFA
A1AA_RABIT
A1AA_HUMAN
A1AA_ORYLA
O96716
O75963
HGPRBMY8

FIG. 6C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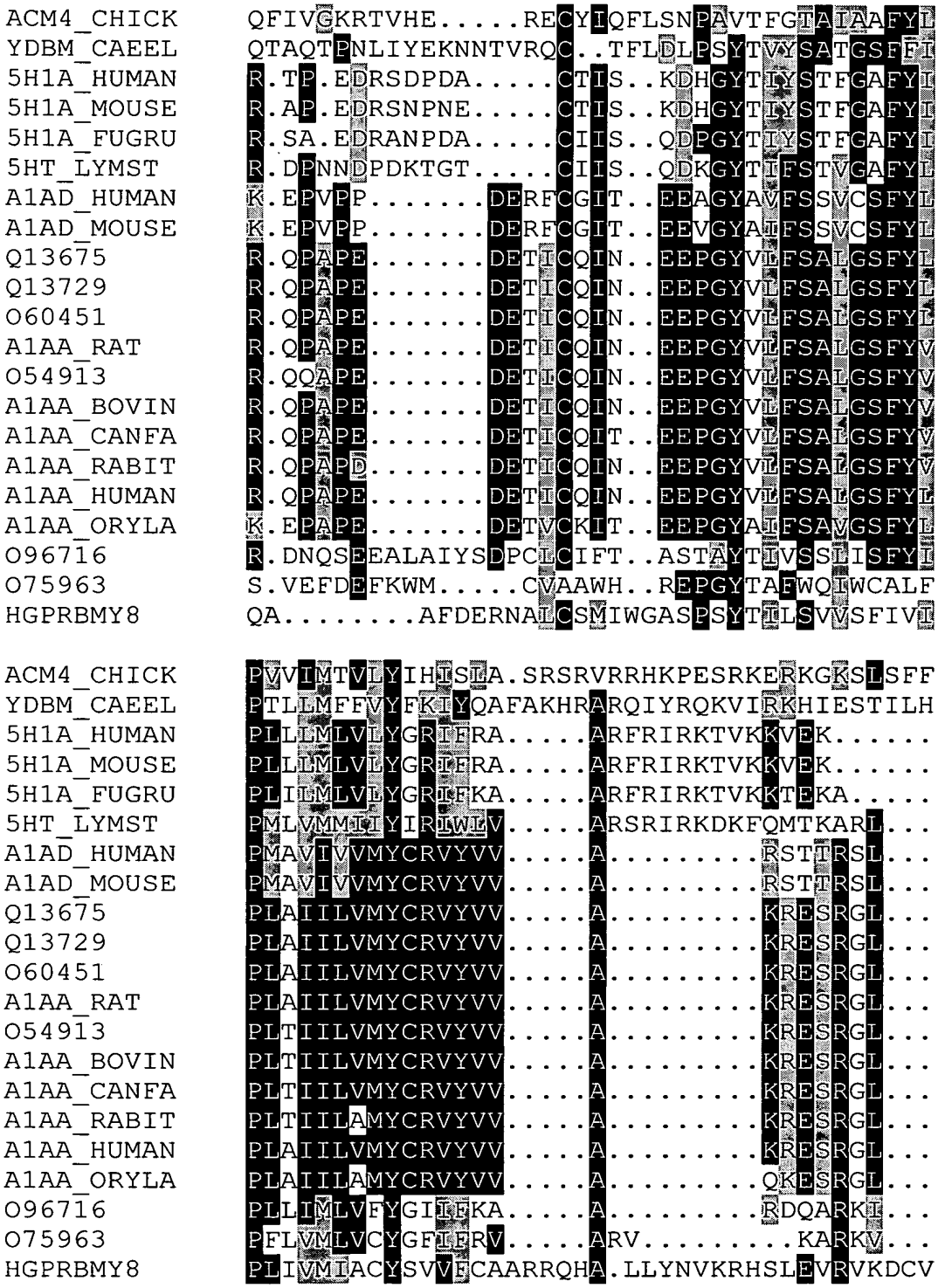
5H1A_HUMAN
5H1A_MOUSE
5H1A_FUGRU
5HT_LYMST
A1AD_HUMAN
A1AD_MOUSE
Q13675
Q13729
O60451
A1AA_RAT
O54913
A1AA_BOVIN
A1AA_CANFA
A1AA_RABIT
A1AA_HUMAN
A1AA_ORYLA
O96716
O75963
HGPRBMY8

FIG. 6D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YDBM_CAEEL
5H1A_HUMAN
5H1A_MOUSE
5H1A_FUGRU
5HT_LYMST
A1AD_HUMAN
A1AD_MOUSE
Q13675
Q13729
O60451
A1AA_RAT
O54913
A1AA_BOVIN
A1AA_CANFA
A1AA_RABIT
A1AA_HUMAN
A1AA_ORYLA
O96716
O75963
HGPRBMY8

FIG. 6E

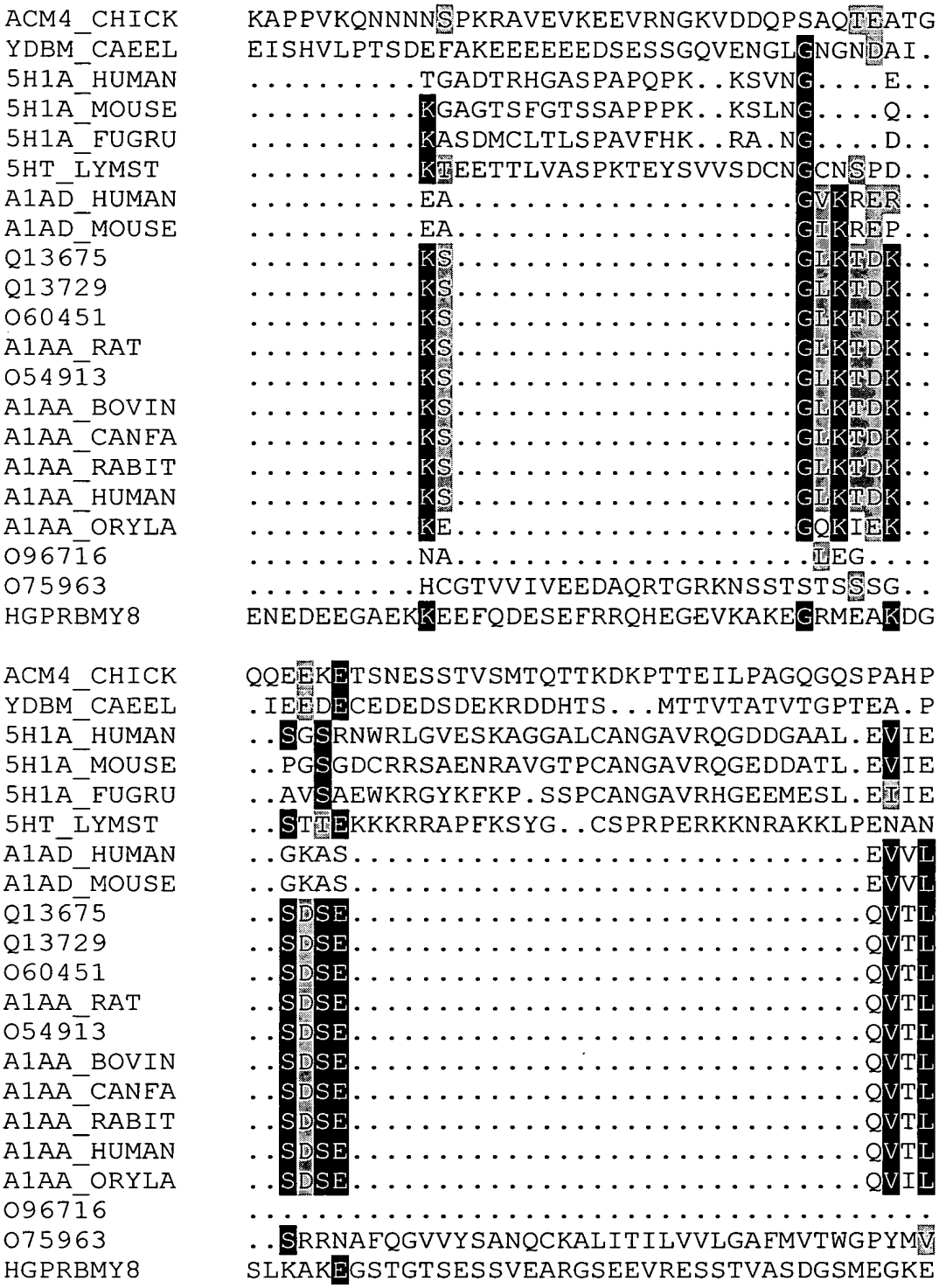

ACM4_CHICK KAPPVKQNNNNSPKRAVEVKEEVRNGKVDDQPSAQTEATG
YDBM_CAEEL EISHVLPTSDEFAKEEEEEEDSESSGQVENGLGNGNDAI.
5H1A_HUMAN .....TGADTRHGASPAPQPK..KSVNG....E..
5H1A_MOUSE .....KGAGTSFGTSSAPPPK..KSLNG....Q..
5H1A_FUGRU .....KASDMCLTLSPAVFHK..RA.NG....D..
5HT_LYMST .....KTEETTLVASPKTEYSVVSDCNGCNSPD..
A1AD_HUMAN .....EA.....GVKRER..
A1AD_MOUSE .....EA.....GIKREP..
Q13675 .....KS.....GLKTDK..
Q13729 .....KS.....GLKTDK..
O60451 .....KS.....GLKTDK..
A1AA_RAT .....KS.....GLKTDK..
O54913 .....KS.....GLKTDK..
A1AA_BOVIN .....KS.....GLKTDK..
A1AA_CANFA .....KS.....GLKTDK..
A1AA_RABIT .....KS.....GLKTDK..
A1AA_HUMAN .....KS.....GLKTDK..
A1AA_ORYLA .....KE.....GQKIEK..
O96716 .....NA.....LEG....
O75963 .....HCGTVVIVEEDAQRTGRKNSSTSTSSSG..
HGPRBMY8 ENEDEEGAEKKEEFQDESEFRRQHEGEVKAKEGRMEAKDG
ACM4_CHICK QQEEKETSNESSTVSMTQTTKDKPTTEILPAGQGQSPAHP
YDBM_CAEEL .IEEDECEDEDSDEKRDDHTS...MTTVTATVTGPTEA.P
5H1A_HUMAN ..SGSRNWRLGVESKAGGALCANGAVRQGDDGAAL.EVIE
5H1A_MOUSE ..PGSGDCRRSAENRAVGTPCANGAVRQGEDDATL.EVIE
5H1A_FUGRU ..AVSAEWKRGYKFKP.SSPCANGAVRHGEEMESL.EIIE
5HT_LYMST ..STTEKKKRRAPFKSYG..CSPRPERKKNRAKKLPENAN
A1AD_HUMAN ..GKAS.....EVVL
A1AD_MOUSE ..GKAS.....EVVL
Q13675 ..SDSE.....QVTL
Q13729 ..SDSE.....QVTL
O60451 ..SDSE.....QVTL
A1AA_RAT ..SDSE.....QVTL
O54913 ..SDSE.....QVTL
A1AA_BOVIN ..SDSE.....QVTL
A1AA_CANFA ..SDSE.....QVTL
A1AA_RABIT ..SDSE.....QVTL
A1AA_HUMAN ..SDSE.....QVTL
A1AA_ORYLA ..SDSE.....QVIL
O96716 .....
O75963 ..SRRNAFQGVVYSANQCKALITILVVLGAFMVTWGPYMV
HGPRBMY8 SLKAKEGSTGTSESSVEARGSEEVRESSTVASDGSMEGKE

FIG. 6F

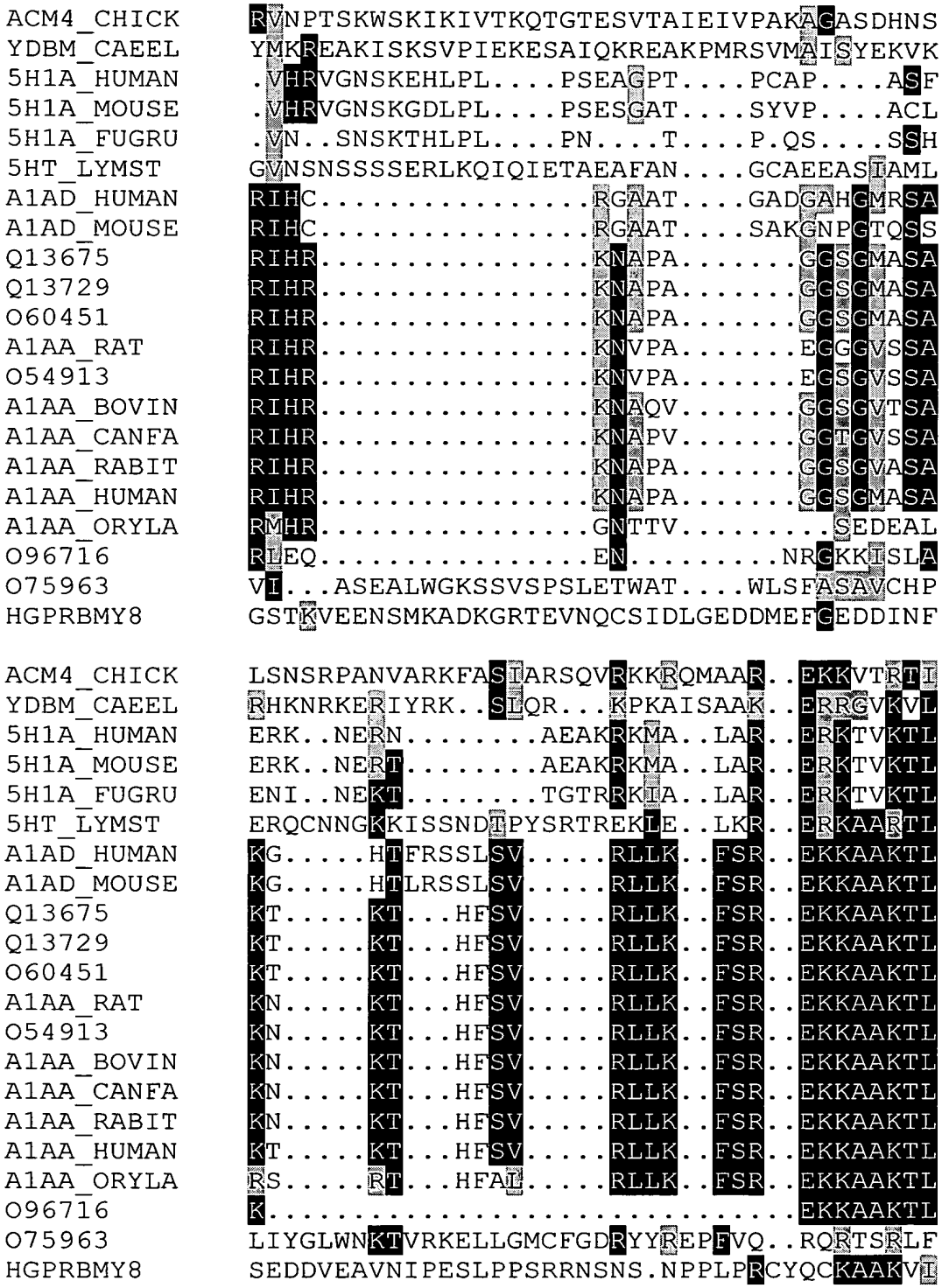

ACM4_CHICK
YDBM_CAEEL
5H1A_HUMAN
5H1A_MOUSE
5H1A_FUGRU
5HT_LYMST
A1AD_HUMAN
A1AD_MOUSE
Q13675
Q13729
O60451
A1AA_RAT
O54913
A1AA_BOVIN
A1AA_CANFA
A1AA_RABIT
A1AA_HUMAN
A1AA_ORYLA
O96716
O75963
HGPRBMY8

FIG. 6G

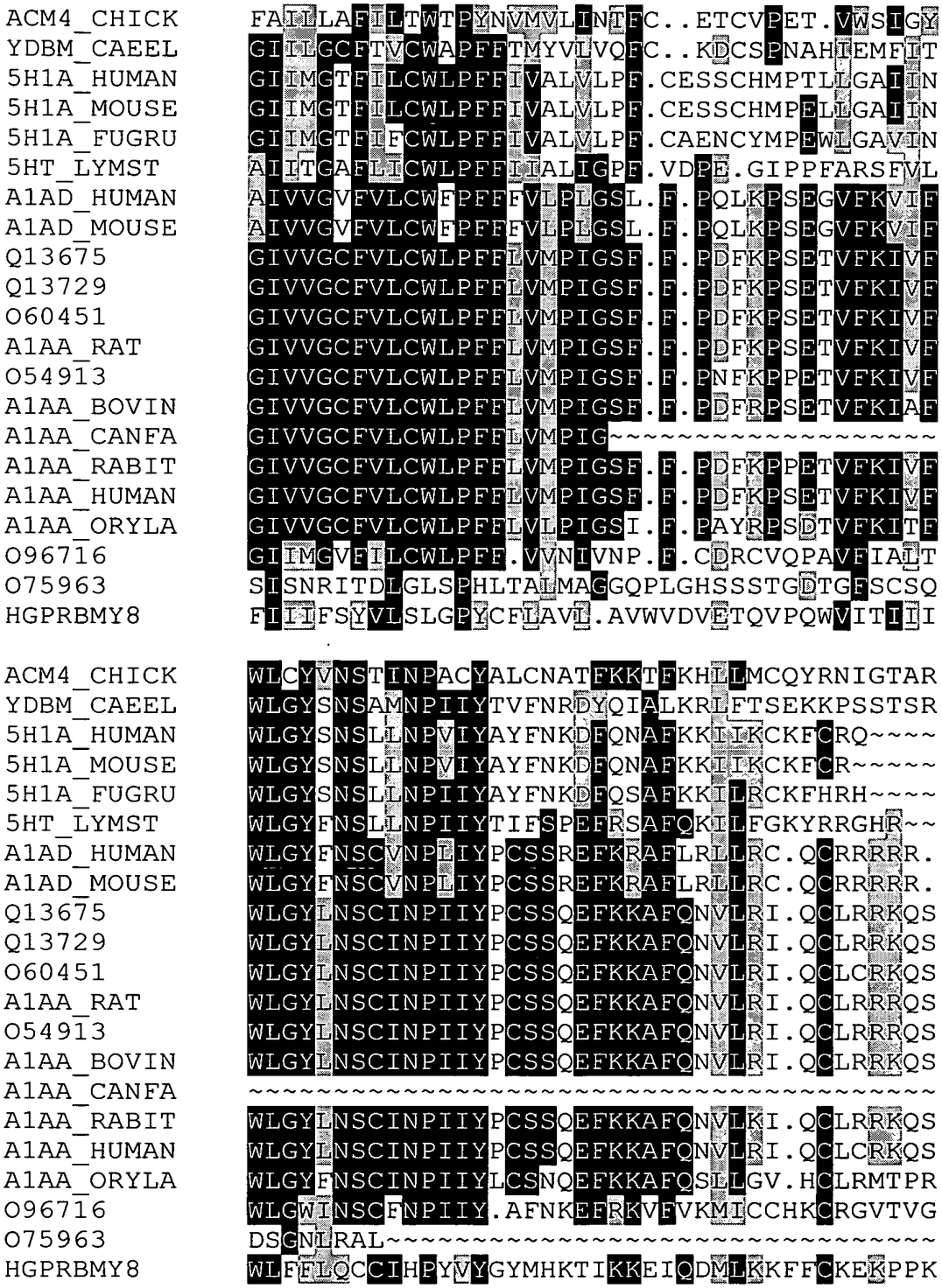

ACM4_CHICK
YDBM_CAEEL
5H1A_HUMAN
5H1A_MOUSE
5H1A_FUGRU
5HT_LYMST
A1AD_HUMAN
A1AD_MOUSE
Q13675
Q13729
O60451
A1AA_RAT
O54913
A1AA_BOVIN
A1AA_CANFA
A1AA_RABIT
A1AA_HUMAN
A1AA_ORYLA
O96716
O75963
HGPRBMY8

FIG. 6H

```
ACM4_CHICK    ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
YDBM_CAEEL    V~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
5H1A_HUMAN    ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
5H1A_MOUSE    ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
5H1A_FUGRU    ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
5HT_LYMST     ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
A1AD_HUMAN    .RRPLWRVY..GHHWRASTSGLRQDCAPSSGDAPPGAPLA
A1AD_MOUSE    .R..LW......PSLRPPLASL..DRRPALRLCPQPAHRT
Q13675        SKH...ALG..YT.LHPPSQAVEGQHKDM.VRIPVGSRET
Q13729        SKH...ALG..YT.LHPPSQAVEGQHKDM.VRIPVGSRET
O60451        SKH...ALG..YT.LHPPSQAVEGQHKDM.VRIPVGSRET
A1AA_RAT      SKH...ALG..YT.LHPPSQALEGQHRDM.VRIPVGSGET
O54913        SKH...ALG..YT.LHPPSQAVEEQHRGM.VRIPVGSGET
A1AA_BOVIN    SKH...TLG..YT.LHAPSHVLEGQHKDL.VRIPVGSAET
A1AA_CANFA    ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
A1AA_RABIT    SKH...ALG..YT.LHAPSQALEGQHKDM.VRIPVGSGET
A1AA_HUMAN    SKH...ALG..YT.LHPPSQAVEGQHKDM.VRIPVGSRET
A1AA_ORYLA    AHHHHLSVG..QSQTQGHSLTISLDSKGAPCRLSPSSSVA
O96716        PNHADLNYDPVAMRLKKRGENANGTVNGDANGKANGNIEA
O75963        ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
HGPRBMY8      EDSHPDLPGTEGGTEGKIVPSYDSATFP~~~~~~~~~~~~

ACM4_CHICK    ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
YDBM_CAEEL    ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
5H1A_HUMAN    ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
5H1A_MOUSE    ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
5H1A_FUGRU    ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
5HT_LYMST     ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
A1AD_HUMAN    LTALPDPD..PEP...PGTPEMQAPVASRRKPPSA...FR
A1AD_MOUSE    PRGSPSPH..CTPR..PGLRRHAGGAGFGLRPSKASLRLR
Q13675        FYRISKTDGVCEWKFFSSMPRGSARITVSKDQSSCTTART
Q13729        FYRISKTDGVCEWKFFSSMPRGSARITVSKDQSSCTTARG
O60451        FYRISKTDGVCEWKFFSSMPRGSARITVSKDQSSCTTARR
A1AA_RAT      FYKISKTDGVCEWKFFSSMPQGSARITVPKDQSACTTARV
O54913        FYKISKTDGVCEWKFFSSMPQGSARITMPKDQSACTTARV
A1AA_BOVIN    FYKISKTDGVCEWKIFSSLPRGSARMAVARDPSACTTARV
A1AA_CANFA    ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
A1AA_RABIT    FYKISKTDGVCEWKFFSSMPRGSARITVPKDQSACTTARV
A1AA_HUMAN    FYRISKTDGVCEWKFFSSMPRGSARITVSKDQSSCTTARV
A1AA_ORYLA    LSRTPSSRDSREWRVFSGGPINSG..PGPTEAGRAKVAKL
O96716        GEGTSSS~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
O75963        ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
HGPRBMY8      ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
```

FIG. 6I

```
ACM4_CHICK    ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
YDBM_CAEEL    ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
5H1A_HUMAN    ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
5H1A_MOUSE    ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
5H1A_FUGRU    ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
5HT_LYMST     ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
A1AD_HUMAN    EWRLLGPFRRPTTQLRAKVSSLSHKIRAGGAQRAEAACAQ
A1AD_MOUSE    EWRLLGPLQRPTTQLRAKVSSLSHKFRSGGARRAETACAL
Q13675        KSRSVTRLECS....GMILAHCN..LRLPGSRDSPASASQ
Q13729        HT.PMT~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
O60451        GMDCRYFTKNC....REHIKHVN..FMMPPWRKGLEC~~~
A1AA_RAT      RSKSFLQVCCCV.GSSAPRPEEN..HQVPTIKIHTISLGE
O54913        RSKSFLQVCCCV.GSSTPRPEEN..HQVPTIKIHTISLGE
A1AA_BOVIN    RSKSFLQVCCCL.GPSTPSHGEN..HQIPTIKIHTISLSE
A1AA_CANFA    ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
A1AA_RABIT    RSKSFLQVCCCV.GPSTPNPGEN..HQVPTIKIHTISLSE
A1AA_HUMAN    RSKSFLQVCCCV.GPSTPSLDKN..HQVPTIKVHTISLSE
A1AA_ORYLA    CNKSLHRTCCCILRARTPTQDPAPLGDLPTIKIHQLSLSE
O96716        ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
O75963        ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
HGPRBMY8      ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~

ACM4_CHICK    ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
YDBM_CAEEL    ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
5H1A_HUMAN    ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
5H1A_MOUSE    ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
5H1A_FUGRU    ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
5HT_LYMST     ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
A1AD_HUMAN    RSEVEAVSLGVPHEVAEGATCQAYELADYSNLRETDI~~~
A1AD_MOUSE    RSEVEAVSLNVPQDGAEAVICQAYEPGDLSNLRETDI~~~
Q13675        AAGTTGDVPPGRRHQAQLIFVFLVETGFHHVGQDDLDLLT
Q13729        ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
O60451        ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
A1AA_RAT      NGEEV~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
O54913        NGEEV~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
A1AA_BOVIN    NGEEV~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
A1AA_CANFA    ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
A1AA_RABIT    NGEEV~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
A1AA_HUMAN    NGEEV~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
A1AA_ORYLA    KGESV~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
O96716        ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
O75963        ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
HGPRBMY8      ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
```

FIG. 6J

```
ACM4_CHICK    ~
YDBM_CAEEL    ~
5H1A_HUMAN    ~
5H1A_MOUSE    ~
5H1A_FUGRU    ~
5HT_LYMST     ~
A1AD_HUMAN    ~
A1AD_MOUSE    ~
Q13675        S
Q13729        ~
O60451        ~
A1AA_RAT      ~
O54913        ~
A1AA_BOVIN    ~
A1AA_CANFA    ~
A1AA_RABIT    ~
A1AA_HUMAN    ~
A1AA_ORYLA    ~
O96716        ~
O75963        ~
HGPRBMY8      ~
```

FIG. 7

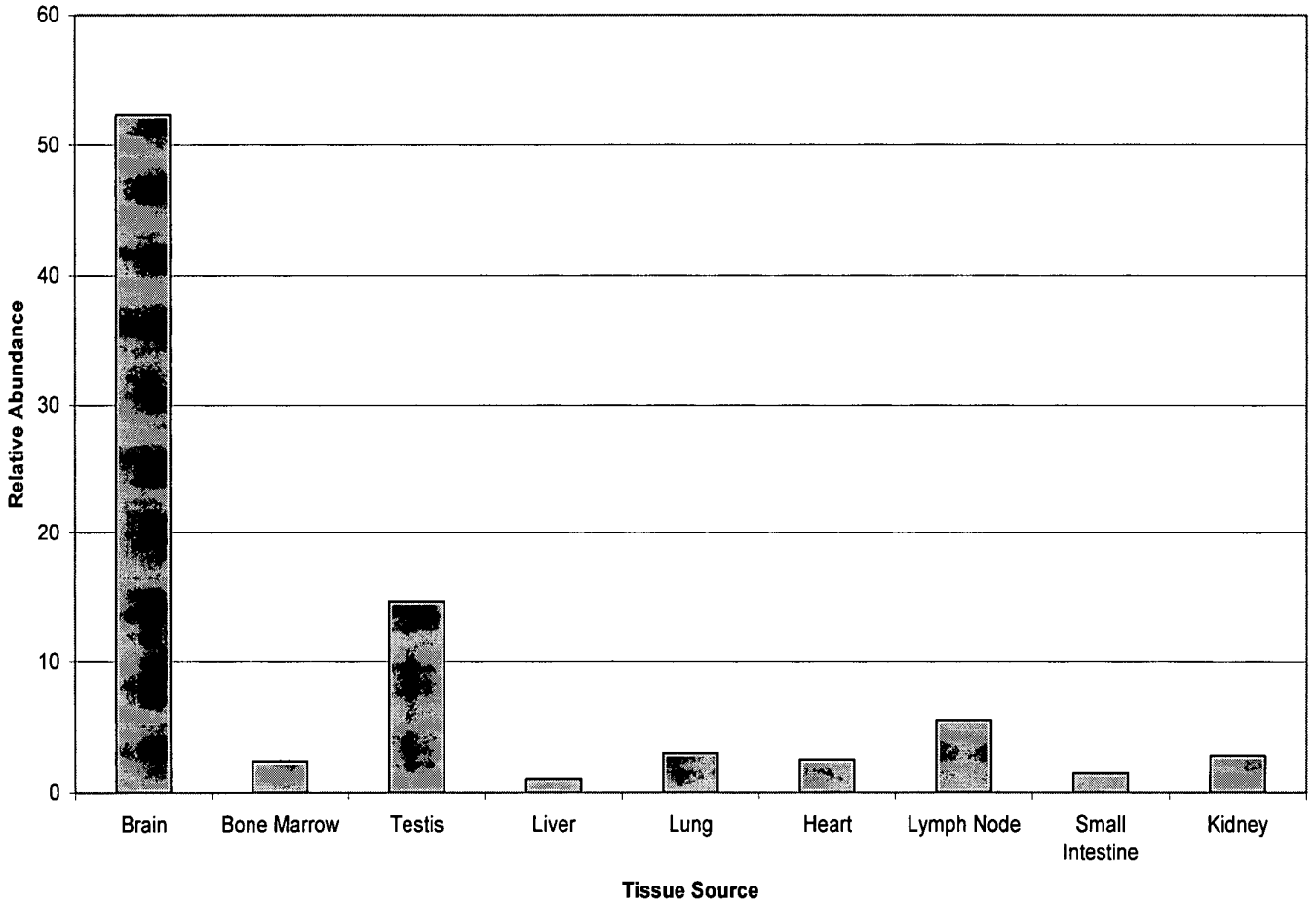

60
50
40
30
20
10
0
Relative Abundance
Brain
Bone Marrow
Testis
Liver
Lung
Heart
Lymph Node
Small Intestine
Kidney
Tissue Source

FIG. 8

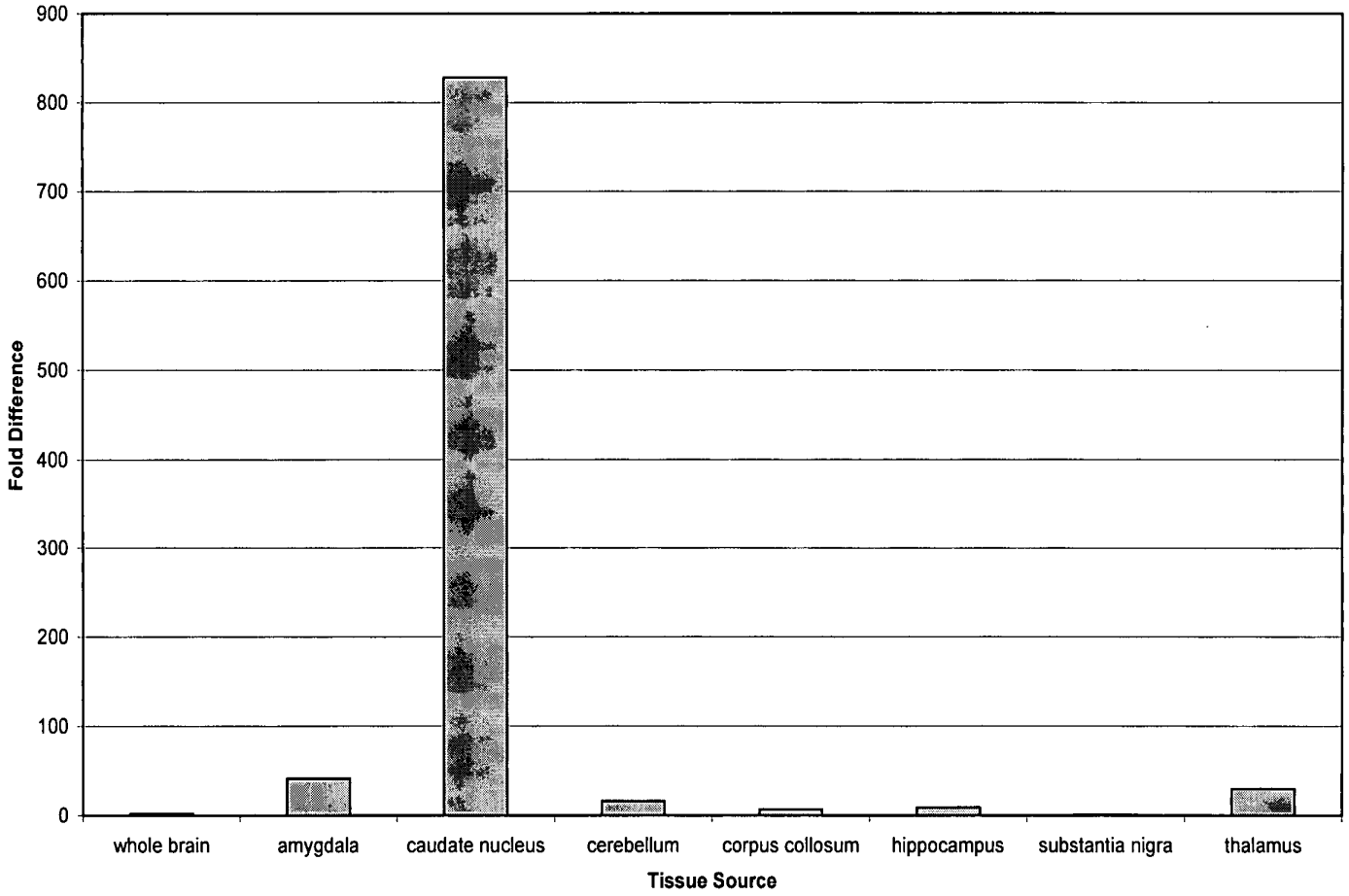

900
800
700
600
500
400
300
200
100
0
Fold Difference
whole brain
amygdala
caudate nucleus
cerebellum
corpus collosum
hippocampus
substantia nigra
thalamus
Tissue Source

FIG. 9

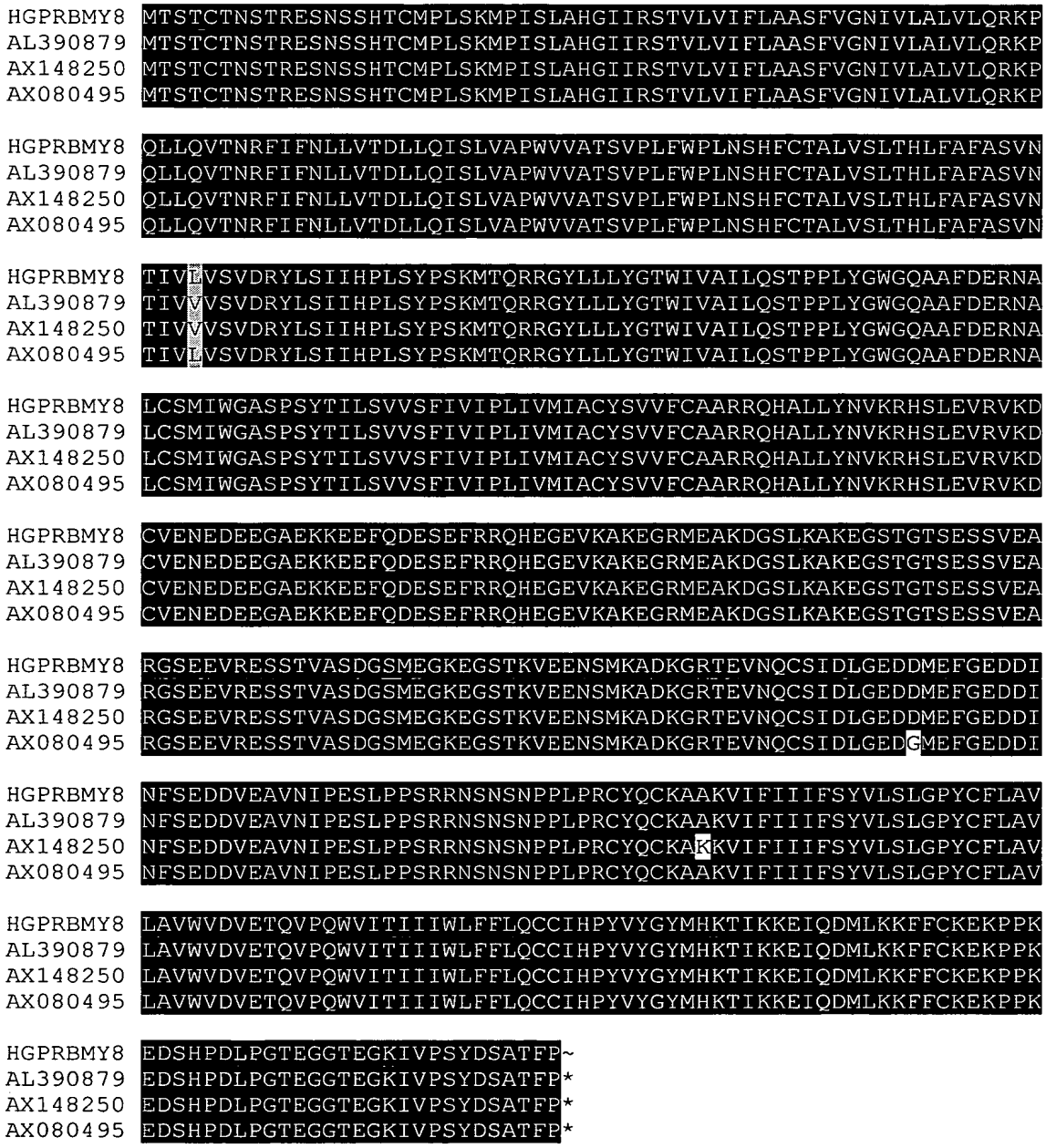

HGPRBMY8 MTSTCTNSTRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKP
AL390879 MTSTCTNSTRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKP
AX148250 MTSTCTNSTRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKP
AX080495 MTSTCTNSTRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKP
HGPRBMY8 QLLQVTNRFIFNLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVN
AL390879 QLLQVTNRFIFNLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVN
AX148250 QLLQVTNRFIFNLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVN
AX080495 QLLQVTNRFIFNLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVN
HGPRBMY8 TIVLVSVDRYLSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNA
AL390879 TIVVVSVDRYLSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNA
AX148250 TIVVVSVDRYLSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNA
AX080495 TIVLVSVDRYLSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNA
HGPRBMY8 LCSMIWGASPSYTILSVVSFIVIPLIVMIACYSVVFCAARRQHALLYNVKRHSLEVRVKD
AL390879 LCSMIWGASPSYTILSVVSFIVIPLIVMIACYSVVFCAARRQHALLYNVKRHSLEVRVKD
AX148250 LCSMIWGASPSYTILSVVSFIVIPLIVMIACYSVVFCAARRQHALLYNVKRHSLEVRVKD
AX080495 LCSMIWGASPSYTILSVVSFIVIPLIVMIACYSVVFCAARRQHALLYNVKRHSLEVRVKD
HGPRBMY8 CVENEDEEGAEKKEEFQDESEFRRQHEGEVKAKEGRMEAKDGSLKAKEGSTGTSESSVEA
AL390879 CVENEDEEGAEKKEEFQDESEFRRQHEGEVKAKEGRMEAKDGSLKAKEGSTGTSESSVEA
AX148250 CVENEDEEGAEKKEEFQDESEFRRQHEGEVKAKEGRMEAKDGSLKAKEGSTGTSESSVEA
AX080495 CVENEDEEGAEKKEEFQDESEFRRQHEGEVKAKEGRMEAKDGSLKAKEGSTGTSESSVEA
HGPRBMY8 RGSEEVRESSTVASDGSMEGKEGSTKVEENSMKADKGRTEVNQCSIDLGEDDMEFGEDDI
AL390879 RGSEEVRESSTVASDGSMEGKEGSTKVEENSMKADKGRTEVNQCSIDLGEDDMEFGEDDI
AX148250 RGSEEVRESSTVASDGSMEGKEGSTKVEENSMKADKGRTEVNQCSIDLGEDDMEFGEDDI
AX080495 RGSEEVRESSTVASDGSMEGKEGSTKVEENSMKADKGRTEVNQCSIDLGEDGMEFGEDDI
HGPRBMY8 NFSEDDVEAVNIPESLPPSRRNSNSNPPLPRCYQCKAAKVIFIIIFSYVLSLGPYCFLAV
AL390879 NFSEDDVEAVNIPESLPPSRRNSNSNPPLPRCYQCKAAKVIFIIIFSYVLSLGPYCFLAV
AX148250 NFSEDDVEAVNIPESLPPSRRNSNSNPPLPRCYQCKAKKVIFIIIFSYVLSLGPYCFLAV
AX080495 NFSEDDVEAVNIPESLPPSRRNSNSNPPLPRCYQCKAAKVIFIIIFSYVLSLGPYCFLAV
HGPRBMY8 LAVWVDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQDMLKKFFCKEKPPK
AL390879 LAVWVDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQDMLKKFFCKEKPPK
AX148250 LAVWVDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQDMLKKFFCKEKPPK
AX080495 LAVWVDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQDMLKKFFCKEKPPK
HGPRBMY8 EDSHPDLPGTEGGTEGKIVPSYDSATFP~
AL390879 EDSHPDLPGTEGGTEGKIVPSYDSATFP*
AX148250 EDSHPDLPGTEGGTEGKIVPSYDSATFP*
AX080495 EDSHPDLPGTEGGTEGKIVPSYDSATFP*

FIG. 10A

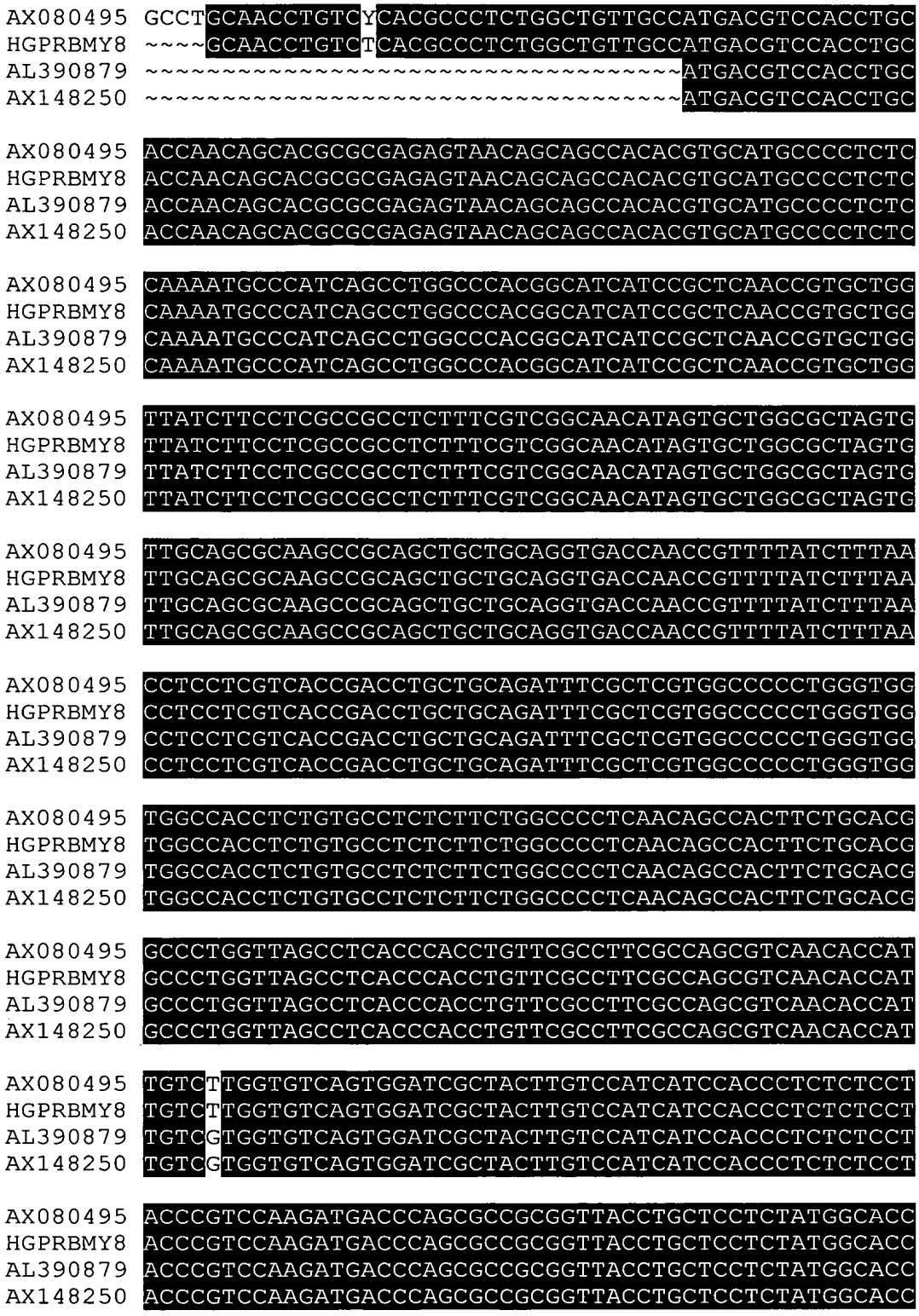

AX080495 GCCTGCAACCTGTCYCACGCCCTCTGGCTGTTGCCATGACGTCCACCTGC
HGPRBMY8 ~~~~GCAACCTGTCTCACGCCCTCTGGCTGTTGCCATGACGTCCACCTGC
AL390879 ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ATGACGTCCACCTGC
AX148250 ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ATGACGTCCACCTGC
AX080495 ACCAACAGCACGCGCGAGAGTAACAGCAGCCACACGTGCATGCCCCTCTC
HGPRBMY8 ACCAACAGCACGCGCGAGAGTAACAGCAGCCACACGTGCATGCCCCTCTC
AL390879 ACCAACAGCACGCGCGAGAGTAACAGCAGCCACACGTGCATGCCCCTCTC
AX148250 ACCAACAGCACGCGCGAGAGTAACAGCAGCCACACGTGCATGCCCCTCTC
AX080495 CAAAATGCCCATCAGCCTGGCCCACGGCATCATCCGCTCAACCGTGCTGG
HGPRBMY8 CAAAATGCCCATCAGCCTGGCCCACGGCATCATCCGCTCAACCGTGCTGG
AL390879 CAAAATGCCCATCAGCCTGGCCCACGGCATCATCCGCTCAACCGTGCTGG
AX148250 CAAAATGCCCATCAGCCTGGCCCACGGCATCATCCGCTCAACCGTGCTGG
AX080495 TTATCTTCCTCGCCGCCTCTTTCGTCGGCAACATAGTGCTGGCGCTAGTG
HGPRBMY8 TTATCTTCCTCGCCGCCTCTTTCGTCGGCAACATAGTGCTGGCGCTAGTG
AL390879 TTATCTTCCTCGCCGCCTCTTTCGTCGGCAACATAGTGCTGGCGCTAGTG
AX148250 TTATCTTCCTCGCCGCCTCTTTCGTCGGCAACATAGTGCTGGCGCTAGTG
AX080495 TTGCAGCGCAAGCCGCAGCTGCTGCAGGTGACCAACCGTTTTATCTTTAA
HGPRBMY8 TTGCAGCGCAAGCCGCAGCTGCTGCAGGTGACCAACCGTTTTATCTTTAA
AL390879 TTGCAGCGCAAGCCGCAGCTGCTGCAGGTGACCAACCGTTTTATCTTTAA
AX148250 TTGCAGCGCAAGCCGCAGCTGCTGCAGGTGACCAACCGTTTTATCTTTAA
AX080495 CCTCCTCGTCACCGACCTGCTGCAGATTTCGCTCGTGGCCCCCTGGGTGG
HGPRBMY8 CCTCCTCGTCACCGACCTGCTGCAGATTTCGCTCGTGGCCCCCTGGGTGG
AL390879 CCTCCTCGTCACCGACCTGCTGCAGATTTCGCTCGTGGCCCCCTGGGTGG
AX148250 CCTCCTCGTCACCGACCTGCTGCAGATTTCGCTCGTGGCCCCCTGGGTGG
AX080495 TGGCCACCTCTGTGCCTCTCTTCTGGCCCCTCAACAGCCACTTCTGCACG
HGPRBMY8 TGGCCACCTCTGTGCCTCTCTTCTGGCCCCTCAACAGCCACTTCTGCACG
AL390879 TGGCCACCTCTGTGCCTCTCTTCTGGCCCCTCAACAGCCACTTCTGCACG
AX148250 TGGCCACCTCTGTGCCTCTCTTCTGGCCCCTCAACAGCCACTTCTGCACG
AX080495 GCCCTGGTTAGCCTCACCCACCTGTTCGCCTTCGCCAGCGTCAACACCAT
HGPRBMY8 GCCCTGGTTAGCCTCACCCACCTGTTCGCCTTCGCCAGCGTCAACACCAT
AL390879 GCCCTGGTTAGCCTCACCCACCTGTTCGCCTTCGCCAGCGTCAACACCAT
AX148250 GCCCTGGTTAGCCTCACCCACCTGTTCGCCTTCGCCAGCGTCAACACCAT
AX080495 TGTCTTGGTGTCAGTGGATCGCTACTTGTCCATCATCCACCCTCTCTCCT
HGPRBMY8 TGTCTTGGTGTCAGTGGATCGCTACTTGTCCATCATCCACCCTCTCTCCT
AL390879 TGTCGTGGTGTCAGTGGATCGCTACTTGTCCATCATCCACCCTCTCTCCT
AX148250 TGTCGTGGTGTCAGTGGATCGCTACTTGTCCATCATCCACCCTCTCTCCT
AX080495 ACCCGTCCAAGATGACCCAGCGCCGCGGTTACCTGCTCCTCTATGGCACC
HGPRBMY8 ACCCGTCCAAGATGACCCAGCGCCGCGGTTACCTGCTCCTCTATGGCACC
AL390879 ACCCGTCCAAGATGACCCAGCGCCGCGGTTACCTGCTCCTCTATGGCACC
AX148250 ACCCGTCCAAGATGACCCAGCGCCGCGGTTACCTGCTCCTCTATGGCACC

FIG. 10B

```
AX080495 TGGATTGTGGCCATCCTGCAGAGCACTCCTCCACTCTACGGCTGGGGCCA
HGPRBMY8 TGGATTGTGGCCATCCTGCAGAGCACTCCTCCACTCTACGGCTGGGGCCA
AL390879 TGGATTGTGGCCATCCTGCAGAGCACTCCTCCACTCTACGGCTGGGGCCA
AX148250 TGGATTGTGGCCATCCTGCAGAGCACTCCTCCACTCTACGGCTGGGGCCA

AX080495 GGCTGCCTTTGATGAGCGCAATGCTCTCTGCTCCATGATCTGGGGGGCCA
HGPRBMY8 GGCTGCCTTTGATGAGCGCAATGCTCTCTGCTCCATGATCTGGGGGGCCA
AL390879 GGCTGCCTTTGATGAGCGCAATGCTCTCTGCTCCATGATCTGGGGGGCCA
AX148250 GGCTGCCTTTGATGAGCGCAATGCTCTCTGCTCCATGATCTGGGGGGCCA

AX080495 GCCCCAGCTACACTATTCTCAGCGTGGTGTCCTTCATCGTCATTCCACTG
HGPRBMY8 GCCCCAGCTACACTATTCTCAGCGTGGTGTCCTTCATCGTCATTCCACTG
AL390879 GCCCCAGCTACACTATTCTCAGCGTGGTGTCCTTCATCGTCATTCCACTG
AX148250 GCCCCAGCTACACTATTCTCAGCGTGGTGTCCTTCATCGTCATTCCACTG

AX080495 ATTGTCATGATTGCCTGCTACTCCGTGGTGTTCTGTGCAGCCCGGAGGCA
HGPRBMY8 ATTGTCATGATTGCCTGCTACTCCGTGGTGTTCTGTGCAGCCCGGAGGCA
AL390879 ATTGTCATGATTGCCTGCTACTCCGTGGTGTTCTGTGCAGCCCGGAGGCA
AX148250 ATTGTCATGATTGCCTGCTACTCCGTGGTGTTCTGTGCAGCCCGGAGGCA

AX080495 GCATGCTCTGCTGTACAATGTCAAGAGACACAGCTTGGAAGTGCGAGTCA
HGPRBMY8 GCATGCTCTGCTGTACAATGTCAAGAGACACAGCTTGGAAGTGCGAGTCA
AL390879 GCATGCTCTGCTGTACAATGTCAAGAGACACAGCTTGGAAGTGCGAGTCA
AX148250 GCATGCTCTGCTGTACAATGTCAAGAGACACAGCTTGGAAGTGCGAGTCA

AX080495 AGGACTGTGTGGAGAATGAGGATGAAGAGGGAGCAGAGAAGAAGGAGGAG
HGPRBMY8 AGGACTGTGTGGAGAATGAGGATGAAGAGGGAGCAGAGAAGAAGGAGGAG
AL390879 AGGACTGTGTGGAGAATGAGGATGAAGAGGGAGCAGAGAAGAAGGAGGAG
AX148250 AGGACTGTGTGGAGAATGAGGATGAAGAGGGAGCAGAGAAGAAGGAGGAG

AX080495 TTCCAGGATGAGAGTGAGTTTCGCCGCCAGCATGAAGGTGAGGTCAAGGC
HGPRBMY8 TTCCAGGATGAGAGTGAGTTTCGCCGCCAGCATGAAGGTGAGGTCAAGGC
AL390879 TTCCAGGATGAGAGTGAGTTTCGCCGCCAGCATGAAGGTGAGGTCAAGGC
AX148250 TTCCAGGATGAGAGTGAGTTTCGCCGCCAGCATGAAGGTGAGGTCAAGGC

AX080495 CAAGGAGGGCAGAATGGAAGCCAAGGACGGCAGCCTGAAGGCCAAGGAAG
HGPRBMY8 CAAGGAGGGCAGAATGGAAGCCAAGGACGGCAGCCTGAAGGCCAAGGAAG
AL390879 CAAGGAGGGCAGAATGGAAGCCAAGGACGGCAGCCTGAAGGCCAAGGAAG
AX148250 CAAGGAGGGCAGAATGGAAGCCAAGGACGGCAGCCTGAAGGCCAAGGAAG

AX080495 GAAGCACGGGGACCAGTGAGAGTAGTGTAGAGGCCAGGGGCAGCGAGGAG
HGPRBMY8 GAAGCACGGGGACCAGTGAGAGTAGTGTAGAGGCCAGGGGCAGCGAGGAG
AL390879 GAAGCACGGGGACCAGTGAGAGTAGTGTAGAGGCCAGGGGCAGCGAGGAG
AX148250 GAAGCACGGGGACCAGTGAGAGTAGTGTAGAGGCCAGGGGCAGCGAGGAG

AX080495 GTCAGAGAGAGCAGCACGGTGGCCAGCGACGGCAGCATGGAGGGTAAGGA
HGPRBMY8 GTCAGAGAGAGCAGCACGGTGGCCAGCGACGGCAGCATGGAGGGTAAGGA
AL390879 GTCAGAGAGAGCAGCACGGTGGCCAGCGACGGCAGCATGGAGGGTAAGGA
AX148250 GTCAGAGAGAGCAGCACGGTGGCCAGCGACGGCAGCATGGAGGGTAAGGA
```

FIG. 10C

```
AX080495 AGGCAGCACCAAAGTTGAGGAGAACAGCATGAAGGCAGACAAGGGTCGCA
HGPRBMY8 AGGCAGCACCAAAGTTGAGGAGAACAGCATGAAGGCAGACAAGGGTCGCA
AL390879 AGGCAGCACCAAAGTTGAGGAGAACAGCATGAAGGCAGACAAGGGTCGCA
AX148250 AGGCAGCACCAAAGTTGAGGAGAACAGCATGAAGGCAGACAAGGGTCGCA

AX080495 CAGAGGTCAACCAGTGCAGCATTGACTTGGGTGAAGATGGCATGGAGTTT
HGPRBMY8 CAGAGGTCAACCAGTGCAGCATTGACTTGGGTGAAGATGACATGGAGTTT
AL390879 CAGAGGTCAACCAGTGCAGCATTGACTTGGGTGAAGATGACATGGAGTTT
AX148250 CAGAGGTCAACCAGTGCAGCATTGACTTGGGTGAAGATGACATGGAGTTT

AX080495 GGTGAAGACGACATCAATTTCAGTGAGGATGACGTCGAGGCAGTGAACAT
HGPRBMY8 GGTGAAGACGACATCAATTTCAGTGAGGATGACGTCGAGGCAGTGAACAT
AL390879 GGTGAAGACGACATCAATTTCAGTGAGGATGACGTCGAGGCAGTGAACAT
AX148250 GGTGAAGACGACATCAATTTCAGTGAGGATGACGTCGAGGCAGTGAACAT

AX080495 CCCGGAGAGCCTCCCACCCAGTCGTCGTAACAGCAACAGCAACCCTCCTC
HGPRBMY8 CCCGGAGAGCCTCCCACCCAGTCGTCGTAACAGCAACAGCAACCCTCCTC
AL390879 CCCGGAGAGCCTCCCACCCAGTCGTCGTAACAGCAACAGCAACCCTCCTC
AX148250 CCCGGAGAGCCTCCCACCCAGTCGTCGTAACAGCAACAGCAACCCTCCTC

AX080495 TGCCCAGGTGCTACCAGTGCAAAGCTGCTAAAGTGATCTTCATCATCATT
HGPRBMY8 TGCCCAGGTGCTACCAGTGCAAAGCTGCTAAAGTGATCTTCATCATCATT
AL390879 TGCCCAGGTGCTACCAGTGCAAAGCTGCTAAAGTGATCTTCATCATCATT
AX148250 TGCCCAGGTGCTACCAGTGCAAAGCTAAAGAAAGTGATCTTCATCATCATT

AX080495 TTCTCCTATGTGCTATCCCTGGGGCCCTACTGCTTTTTAGCAGTCCTGGC
HGPRBMY8 TTCTCCTATGTGCTATCCCTGGGGCCCTACTGCTTTTTAGCAGTCCTGGC
AL390879 TTCTCCTATGTGCTATCCCTGGGGCCCTACTGCTTTTTAGCAGTCCTGGC
AX148250 TTCTCCTATGTGCTATCCCTGGGGCCCTACTGCTTTTTAGCAGTCCTGGC

AX080495 CGTGTGGGTGGATGTCGAAACCCAGGTACCCCAGTGGGTGATCACCATAA
HGPRBMY8 CGTGTGGGTGGATGTCGAAACCCAGGTACCCCAGTGGGTGATCACCATAA
AL390879 CGTGTGGGTGGATGTCGAAACCCAGGTACCCCAGTGGGTGATCACCATAA
AX148250 CGTGTGGGTGGATGTCGAAACCCAGGTACCCCAGTGGGTGATCACCATAA

AX080495 TCATCTGGCTTTTCTTCCTGCAGTGCTGCATCCACCCCTATGTCTATGGC
HGPRBMY8 TCATCTGGCTTTTCTTCCTGCAGTGCTGCATCCACCCCTATGTCTATGGC
AL390879 TCATCTGGCTTTTCTTCCTGCAGTGCTGCATCCACCCCTATGTCTATGGC
AX148250 TCATCTGGCTTTTCTTCCTGCAGTGCTGCATCCACCCCTATGTCTATGGC

AX080495 TACATGCACAAGACCATTAAGAAGGAAATCCAGGACATGCTGAAGAAGTT
HGPRBMY8 TACATGCACAAGACCATTAAGAAGGAAATCCAGGACATGCTGAAGAAGTT
AL390879 TACATGCACAAGACCATTAAGAAGGAAATCCAGGACATGCTGAAGAAGTT
AX148250 TACATGCACAAGACCATTAAGAAGGAAATCCAGGACATGCTGAAGAAGTT

AX080495 CTTCTGCAAGGAAAAGCCCCCGAAAGAAGATAGCCACCCAGACCTGCCCG
HGPRBMY8 CTTCTGCAAGGAAAAGCCCCCGAAAGAAGATAGCCACCCAGACCTGCCCG
AL390879 CTTCTGCAAGGAAAAGCCCCCGAAAGAAGATAGCCACCCAGACCTGCCCG
AX148250 CTTCTGCAAGGAAAAGCCCCCGAAAGAAGATAGCCACCCAGACCTGCCCG
```

FIG. 10D

```
AX080495 GAACAGAGGGTGGGACTGAAGGCAAGATTGTCCCTTCCTACGATTCTGCT
HGPRBMY8 GAACAGAGGGTGGGACTGAAGGCAAGATTGTCCCTTCCTACGATTCTGCT
AL390879 GAACAGAGGGTGGGACTGAAGGCAAGATTGTCCCTTCCTACGATTCTGCT
AX148250 GAACAGAGGGTGGGACTGAAGGCAAGATTGTCCCTTCCTACGATTCTGCT

AX080495 ACTTTTCCTTGAAGTTAGTTCTAAGGCAAACCTTGAAAATCAGTCCTTCA
HGPRBMY8 ACTTTTCCTTGAAGTTAGTTCTAAGGCAAACCTT~~~~~~~~~~~~~~~~
AL390879 ACTTTTCCTTGA~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
AX148250 ACTTTTCCTTGA~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~

AX080495 GCCACAGCTATTTAGAGCTTTAAAACTACCAGGTTCAATCACTGGTTATG
HGPRBMY8 ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
AL390879 ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
AX148250 ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~

AX080495 CTTTCTGTG
HGPRBMY8 ~~~~~~~~~
AL390879 ~~~~~~~~~
AX148250 ~~~~~~~~~
```

FIG. 11

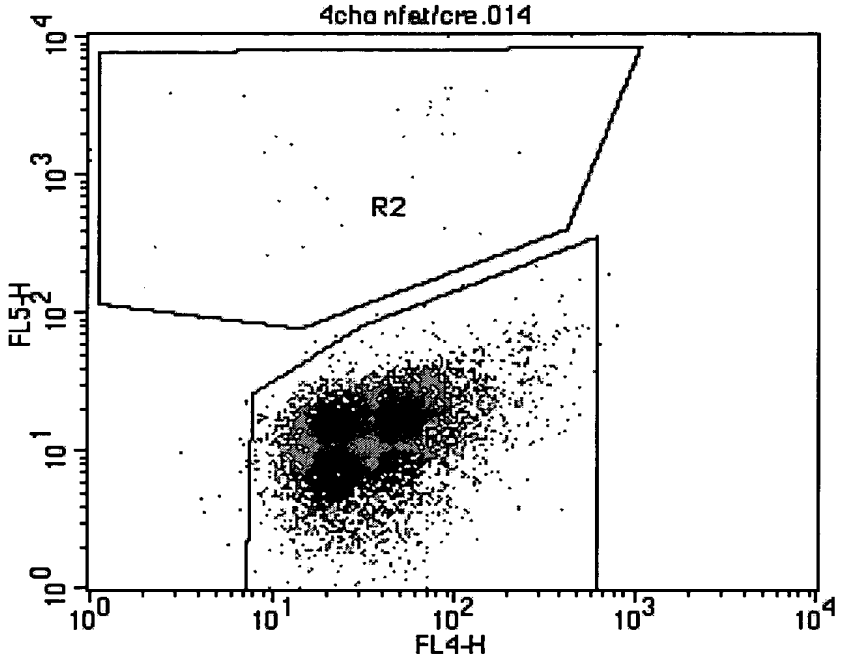

4cho nfat/cre.014
R2
FL5-H
FL4-H
10^0
10^1
10^2
10^3
10^4

FIG. 12

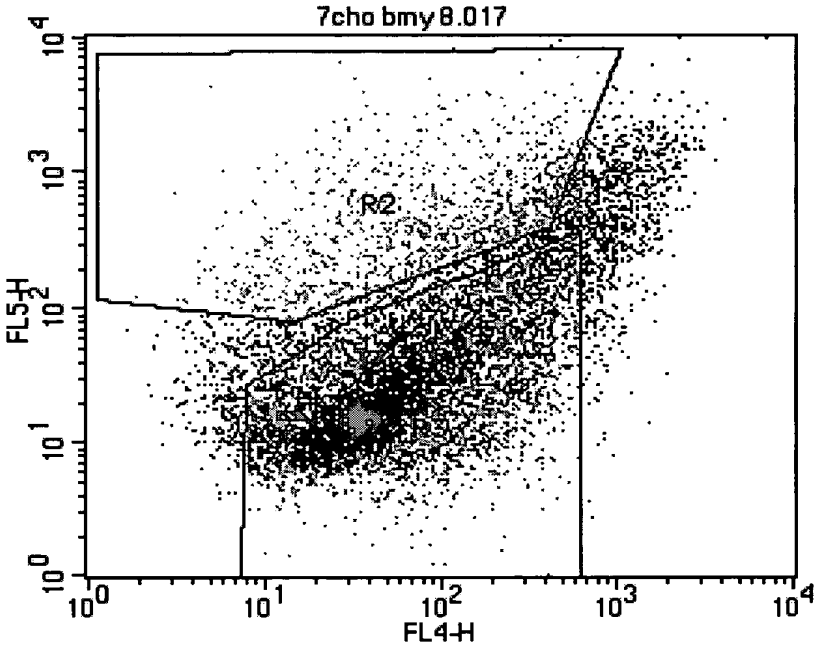

7cho bmy 8.017
R2
FL5-H
FL4-H
10^0
10^1
10^2
10^3
10^4

FIG. 13

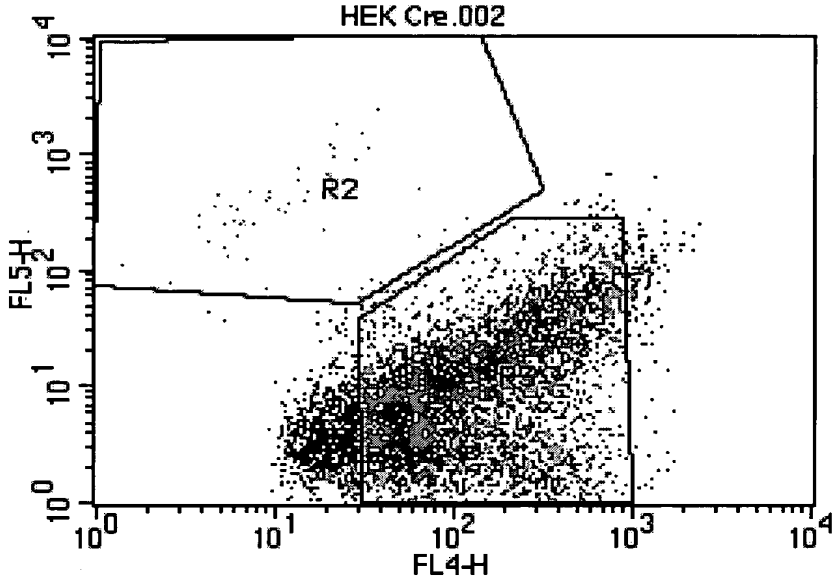

HEK Cre.002
R2
FL5-H
FL4-H
10^0
10^1
10^2
10^3
10^4

FIG. 14

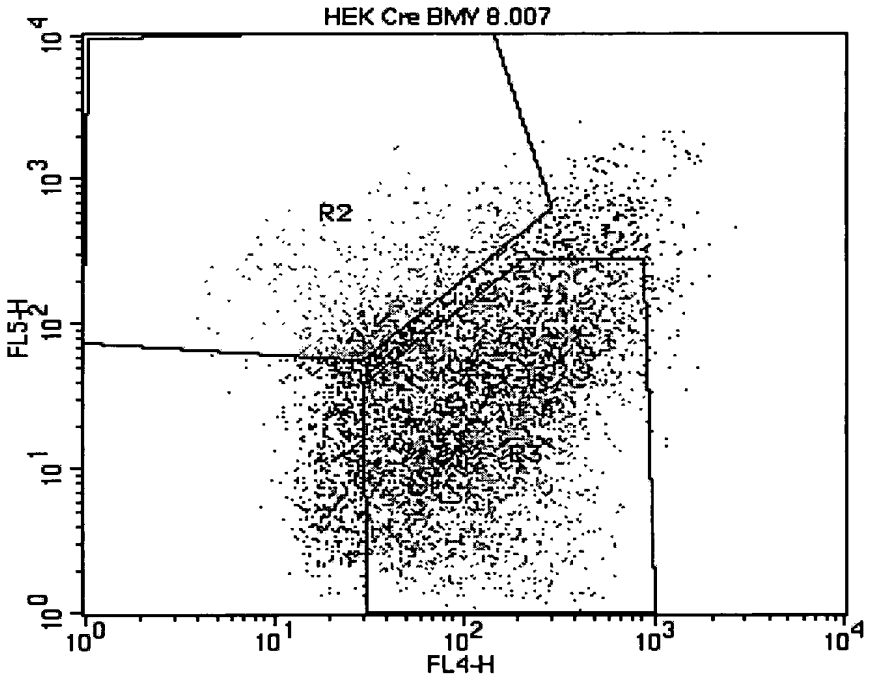
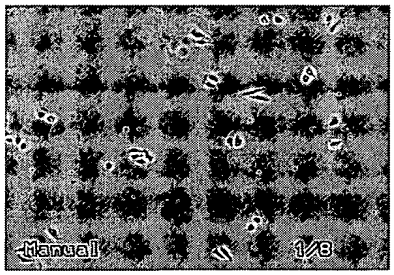
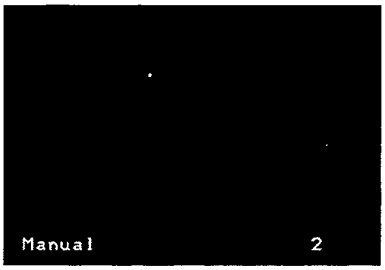

HEK Cre BMY 8.007
R2
FL5-H
FL4-H
10^0
10^1
10^2
10^3
10^4

FIG. 15

a. CHO-NFAT G alpha 15 (Fluorescent vs. Bright Field)





b. CHO-NFAT/ G alpha 15 HGPRBMY8 (Fluorescent vs. Bright Field)

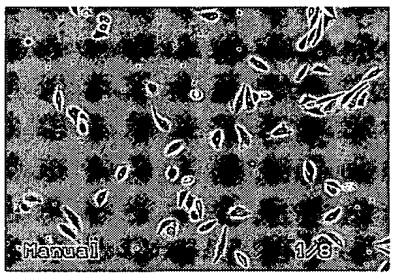
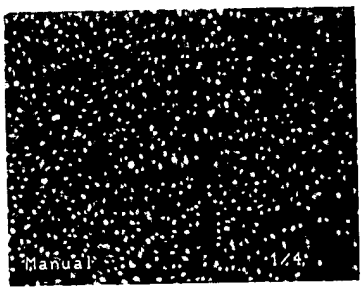
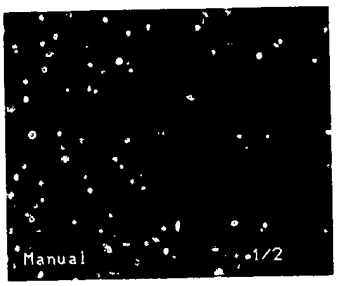


FIG. 16

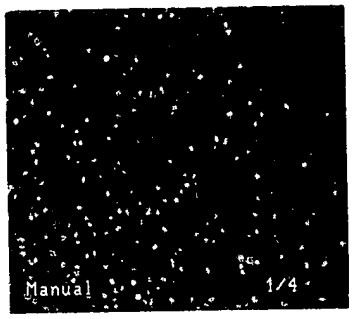
a. CHO-NFAT CRE



b. CHO-NFAT/CRE + FTP



c. CHO-NFAT CRE oGPCR-Intermediate



d. CHO-NFAT/CRE oGPCR high

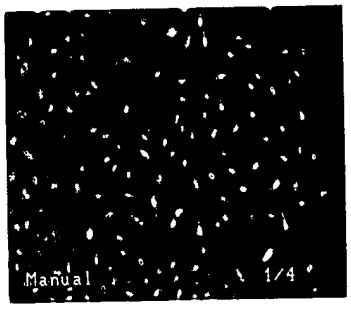


FIG. 17

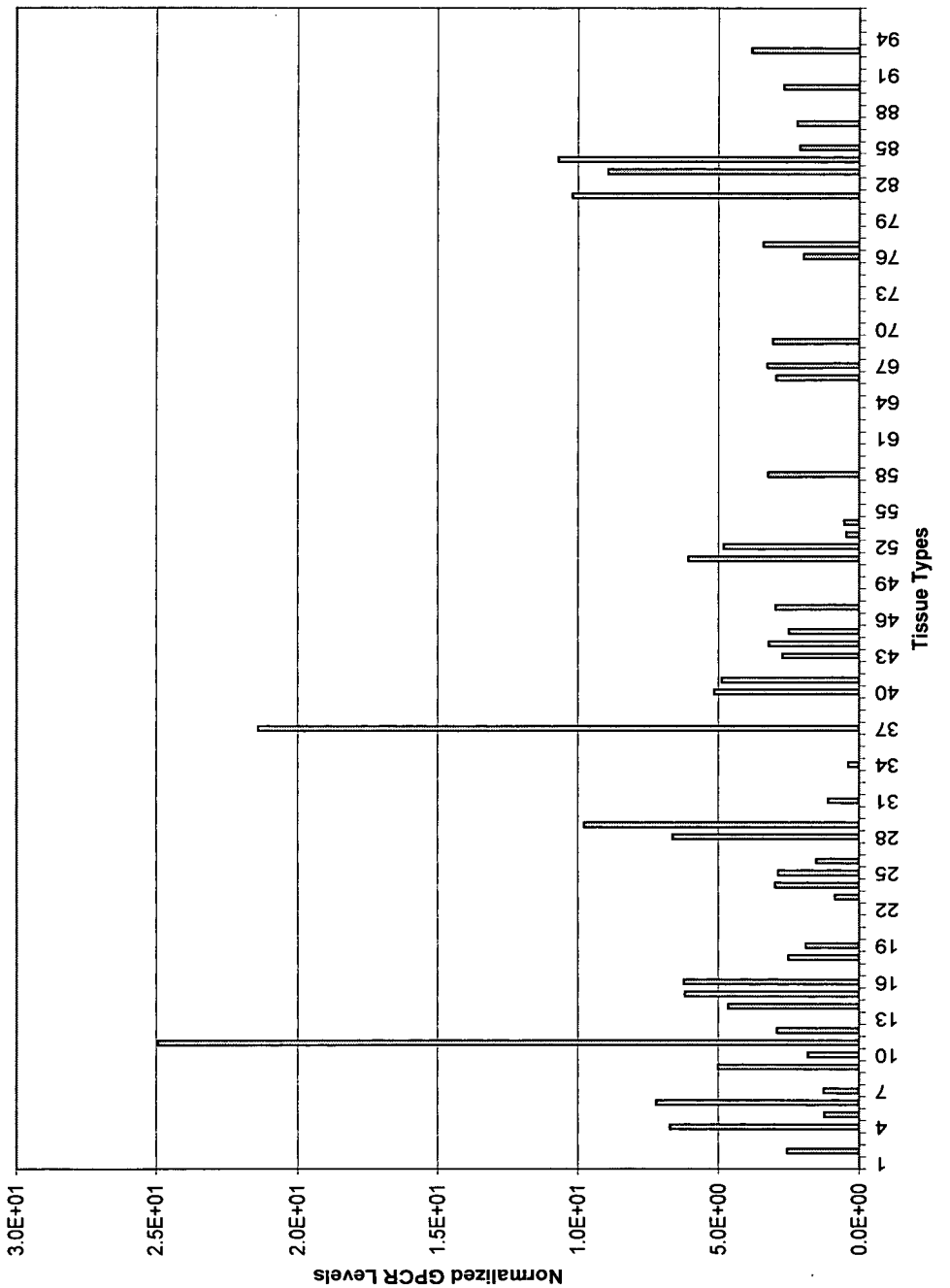

Normalized GPCR Levels
3.0E+01
2.5E+01
2.0E+01
1.5E+01
1.0E+01
5.0E+00
0.0E+00
Tissue Types
1
4
7
10
13
16
19
22
25
28
31
34
37
40
43
46
49
52
55
58
61
64
67
70
73
76
79
82
85
88
91
94

FIG. 18A

```
                .         .         .         .         .         .
  1 ATGACGTCCACCTGCACCAACAGCACGCGCGAGAGTAACAGCAGCCACACGTGCATGCCC   60
  1 M  T  S  T  C  T  N  S  T  R  E  S  N  S  S  H  T  C  M  P    20

                .         .         .         .         .         .
 61 CTCTCCAAAATGCCCATCAGCCTGGCCCACGGCATCATCCGCTCAACCGTGCTGGTTATC   120
 21 L  S  K  M  P  I  S  L  A  H  G  I  I  R  S  T  V  L  V  I    40

                .         .         .         .         .         .
121 TTCCTCGCCGCCTCTTTCGTCGGCAACATAGTGCTGGCGCTAGTGTTGCAGCGCAAGCCG   180
 41 F  L  A  A  S  F  V  G  N  I  V  L  A  L  V  L  Q  R  K  P    60

                .         .         .         .         .         .
181 CAGCTGCTGCAGGTGACCAACCGTTTTATCTTTAACCTCCTCGTCACCGACCTGCTGCAG   240
 61 Q  L  L  Q  V  T  N  R  F  I  F  N  L  L  V  T  D  L  L  Q    80

                .         .         .         .         .         .
241 ATTTCGCTCGTGGCCCCCTGGGTGGTGGCCACCTCTGTGCCTCTCTTCTGGCCCCTCAAC   300
 81 I  S  L  V  A  P  W  V  V  A  T  S  V  P  L  F  W  P  L  N    100

                .         .         .         .         .         .
301 AGCCACTTCTGCACGGCCCTGGTTAGCCTCACCCACCTGTTCGCCTTCGCCAGCGTCAAC   360
101 S  H  F  C  T  A  L  V  S  L  T  H  L  F  A  F  A  S  V  N    120

                .         .         .         .         .         .
361 ACCATTGTCNTGGTGTCAGTGGATCGCTACTTGTCCATCATCCACCCTCTCTCCTACCCG   420
121 T  I  V  X  V  S  V  D  R  Y  L  S  I  I  H  P  L  S  Y  P    140

                .         .         .         .         .         .
421 TCCAAGATGACCCAGCGCCGCGGTTACCTGCTCCTCTATGGCACCTGGATTGTGGCCATC   480
141 S  K  M  T  Q  R  R  G  Y  L  L  L  Y  G  T  W  I  V  A  I    160

                .         .         .         .         .         .
481 CTGCAGAGCACTCCTCCACTCTACGGCTGGGGCCAGGCTGCCTTTGATGAGCGCAATGCT   540
161 L  Q  S  T  P  P  L  Y  G  W  G  Q  A  A  F  D  E  R  N  A    180

                .         .         .         .         .         .
541 CTCTGCTCCATGATCTGGGGGGCCAGCCCCAGCTACACTATTCTCAGCGTGGTGTCCTTC   600
181 L  C  S  M  I  W  G  A  S  P  S  Y  T  I  L  S  V  V  S  F    200

                .         .         .         .         .         .
601 ATCGTCATTCCACTGATTGTCATGATTGCCTGCTACTCCGTGGTGTTCTGTGCAGCCCGG   660
201 I  V  I  P  L  I  V  M  I  A  C  Y  S  V  V  F  C  A  A  R    220

                .         .         .         .         .         .
661 AGGCAGCATGCTCTGCTGTACAATGTCAAGAGACACAGCTTGGAAGTGCGAGTCAAGGAC   720
221 R  Q  H  A  L  L  Y  N  V  K  R  H  S  L  E  V  R  V  K  D    240

                .         .         .         .         .         .
721 TGTGTGGAGAATGAGGATGAAGAGGGAGCAGAGAAGAAGGAGGAGTTCCAGGATGAGAGT   780
241 C  V  E  N  E  D  E  E  G  A  E  K  K  E  E  F  Q  D  E  S    260

                .         .         .         .         .         .
781 GAGTTTCGCCGCCAGCATGAAGGTGAGGTCAAGGCCAAGGAGGGCAGAATGGAAGCCAAG   840
261 E  F  R  R  Q  H  E  G  E  V  K  A  K  E  G  R  M  E  A  K    280

                .         .         .         .         .         .
841 GACGGCAGCCTGAAGGCCAAGGAAGGAAGCACGGGGACCAGTGAGAGTAGTGTAGAGGCC   900
281 D  G  S  L  K  A  K  E  G  S  T  G  T  S  E  S  S  V  E  A    300
```

FIG. 18B

```
                .         .         .         .         .         .
 901  AGGGGCAGCGAGGAGGTCAGAGAGAGCAGCACGGTGGCCAGCGACGGCAGCATGGAGGGT   960
 301  R  G  S  E  E  V  R  E  S  S  T  V  A  S  D  G  S  M  E  G    320

                .         .         .         .         .         .
 961  AAGGAAGGCAGCACCAAAGTTGAGGAGAACAGCATGAAGGCAGACAAGGGTCGCACAGAG   1020
 321  K  E  G  S  T  K  V  E  E  N  S  M  K  A  D  K  G  R  T  E    340

                .         .         .         .         .         .
1021  GTCAACCAGTGCAGCATTGACTTGGGTGAAGATGNCATGGAGTTTGGTGAAGACGACATC   1080
 341  V  N  Q  C  S  I  D  L  G  E  D  X  M  E  F  G  E  D  D  I    360

                .         .         .         .         .         .
1081  AATTTCAGTGAGGATGACGTCGAGGCAGTGAACATCCCGGAGAGCCTCCCACCCAGTCGT   1140
 361  N  F  S  E  D  D  V  E  A  V  N  I  P  E  S  L  P  P  S  R    380

                .         .         .         .         .         .
1141  CGTAACAGCAACAGCAACCCTCCTCTGCCCAGGTGCTACCAGTGCAAAGCTNNNAAAGTG   1200
 381  R  N  S  N  S  N  P  P  L  P  R  C  Y  Q  C  K  A  X  K  V    400

                .         .         .         .         .         .
1201  ATCTTCATCATCATTTTCTCCTATGTGCTATCCCTGGGGCCCTACTGCTTTTTAGCAGTC   1260
 401  I  F  I  I  I  F  S  Y  V  L  S  L  G  P  Y  C  F  L  A  V    420

                .         .         .         .         .         .
1261  CTGGCCGTGTGGGTGGATGTCGAAACCCAGGTACCCCAGTGGGTGATCACCATAATCATC   1320
 421  L  A  V  W  V  D  V  E  T  Q  V  P  Q  W  V  I  T  I  I  I    440

                .         .         .         .         .         .
1321  TGGCTTTTCTTCCTGCAGTGCTGCATCCACCCCTATGTCTATGGCTACATGCACAAGACC   1380
 441  W  L  F  F  L  Q  C  C  I  H  P  Y  V  Y  G  Y  M  H  K  T    460

                .         .         .         .         .         .
1381  ATTAAGAAGGAAATCCAGGACATGCTGAAGAAGTTCTTCTGCAAGGAAAAGCCCCCGAAA   1440
 461  I  K  K  E  I  Q  D  M  L  K  K  F  F  C  K  E  K  P  P  K    480

                .         .         .         .         .         .
1441  GAAGATAGCCACCCAGACCTGCCCGGAACAGAGGGTGGGACTGAAGGCAAGATTGTCCCT   1500
 481  E  D  S  H  P  D  L  P  G  T  E  G  G  T  E  G  K  I  V  P    500

                .         .
1501  TCCTACGATTCTGCTACTTTTCCTTGA  1527
 501  S  Y  D  S  A  T  F  P       508
```

FIG. 19

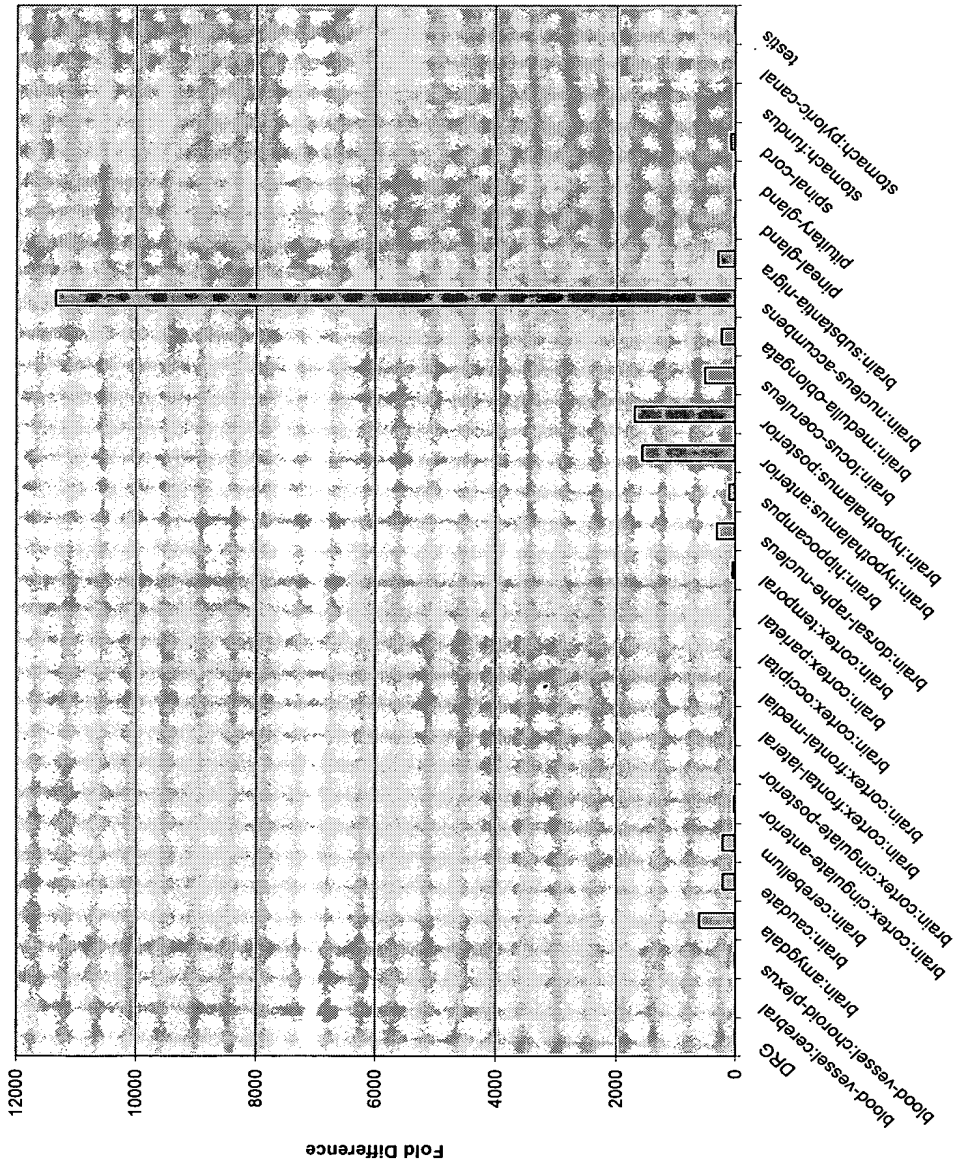

Fold Difference
12000
10000
8000
6000
4000
2000
0
DRG
blood-vessel:cerebral
brain:amygdala
brain:caudate
brain:cerebellum
brain:cortex:cingulate-anterior
brain:cortex:cingulate-posterior
brain:cortex:frontal-lateral
brain:cortex:frontal-medial
brain:cortex:occipital
brain:cortex:temporal
brain:dorsal-raphe-nucleus
brain:hippocampus
brain:hypothalamus:anterior
brain:hypothalamus:posterior
brain:locus-coeruleus
brain:medulla-oblongata
brain:nucleus-accumbens
brain:substantia-nigra
pineal-gland
pituitary-gland
spinal-cord
stomach:fundus
stomach:pyloric-canal
testis

FIG. 20

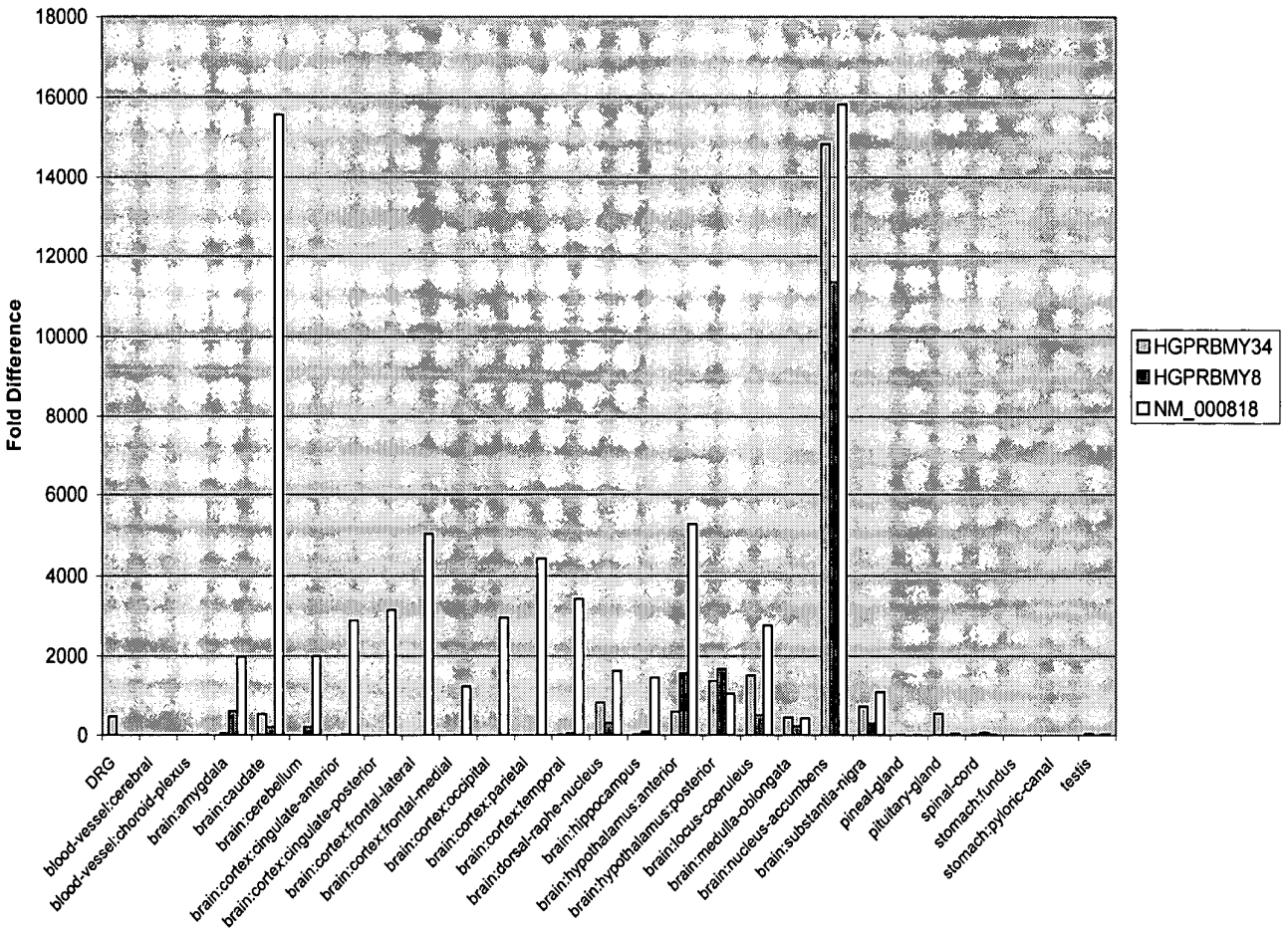

Fold Difference
18000
16000
14000
12000
10000
8000
6000
4000
2000
0
HGPRBMY34
HGPRBMY8
NM_000818
DRG
blood-vessel:cerebral
blood-vessel:choroid-plexus
brain:amygdala
brain:caudate
brain:cerebellum
brain:cortex:cingulate-anterior
brain:cortex:cingulate-posterior
brain:cortex:frontal-lateral
brain:cortex:frontal-medial
brain:cortex:occipital
brain:cortex:parietal
brain:cortex:temporal
brain:dorsal-raphe-nucleus
brain:hippocampus
brain:hypothalamus:anterior
brain:hypothalamus:posterior
brain:locus-coeruleus
brain:medulla-oblongata
brain:nucleus-accumbens
brain:substantia-nigra
pineal-gland
pituitary-gland
spinal-cord
stomach:fundus
stomach:pyloric-canal
testis

FIG. 21

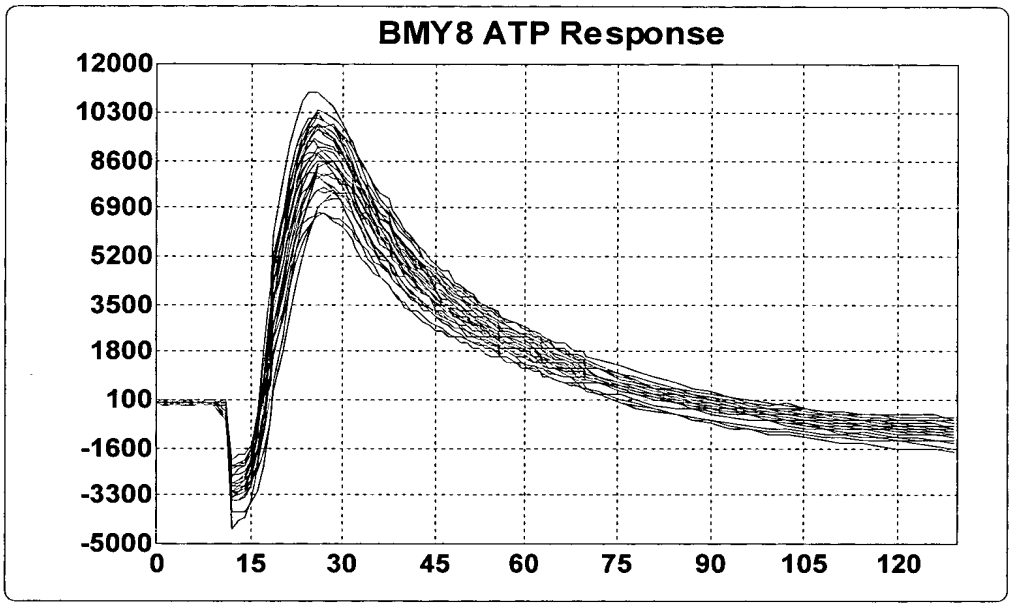
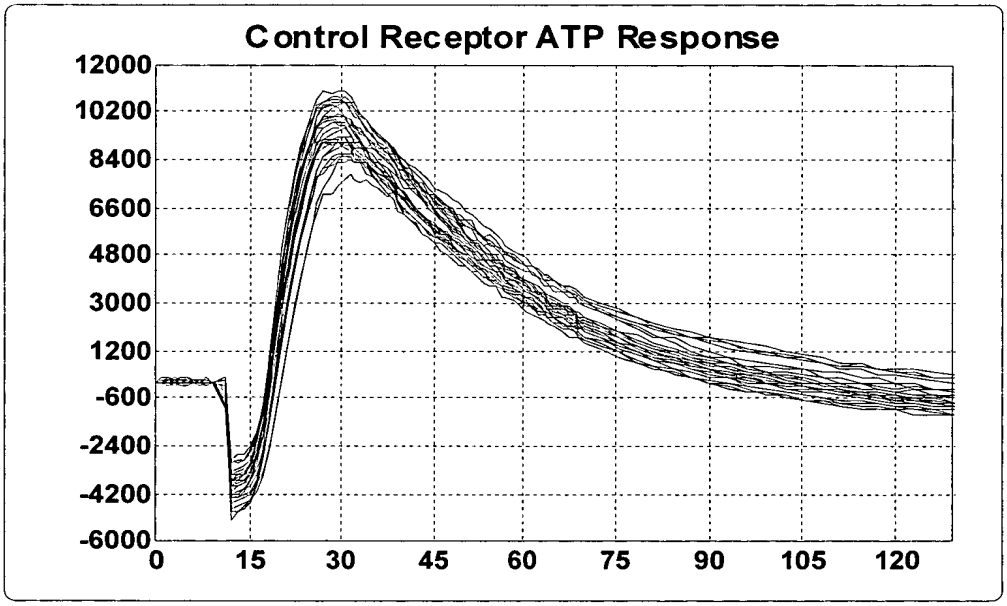

BMY8 ATP Response
12000
10300
8600
6900
5200
3500
1800
100
-1600
-3300
-5000
0
15
30
45
60
75
90
105
120

FIG. 22


Control Receptor ATP Response
12000
10200
8400
6600
4800
3000
1200
-600
-2400
-4200
-6000
0
15
30
45
60
75
90
105
120